

sequence.//4.7e-38:284:85//AC005670

R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25.

Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.4
8:460:58//AL023575

R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18
unordered pieces.//2.5e-21:159:80//AC005081

R-HEMBA1004038//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer
Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC00605

4

R-HEMBA1004042//Homo sapiens clone DJ0968I16, complete sequence.//0.0007
1:263:68//AC006016

R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequen
ce.//8.8e-23:196:69//AC006143

R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 22
88N20, genomic survey sequence.//0.013:162:67//AQ007283

R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protei
n.//7.7e-30:176:96//X04677

R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomi
c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63/
/AC005504

R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3
unordered pieces.//3.5e-61:551:77//AC005484

R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3
unordered pieces.//0.98:275:63//AC004952

R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//I76
237

R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complet
e cds.//1.8e-11:323:63//AF091234

R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:

69//D50918

R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211_P_7, complete sequence.//6.0e-49:491:76//AC003665

R-HEMBA1004133//HS_3229_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003

R-HEMBA1004138//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//3.1e-09:277:66//AL024498

R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence.//0.53:239:61//AL008970

R-HEMBA1004146//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.0e-35:165:88//AC004820

R-HEMBA1004150//CITBI-E1-2517I2.TR CITBI-E1 Homo sapiens genomic clone 2517I2, genomic survey sequence.//0.56:379:59//AQ277616

R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence.//4.6e-49:448:77//AC002429

R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//2.4e-110:563:96//AF067855

R-HEMBA1004199//S.pombe chromosome I cosmid c8A4.//0.73:187:64//Z66569

R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//6.3e-30:293:77//AC004552

R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].//3.0e-64:517:80//S72304

R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.0e-97:303:98//AC005488

R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.6e-116:573:97//U50748

R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes.//5.4e-11:493:60//M37275

R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//6.1e-76:443:86//AF095927

R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence.//1.1e-42:330:83//AC005763

R-HEMBA1004241

R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//1.1e-45:288:85//AP000011

R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.2e-09:516:61//AC004903

R-HEMBA1004264

R-HEMBA1004267//HS_2255_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=0, genomic survey sequence.//8.6e-59:318:95//AQ068854

R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-113:576:96//AC005831

R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence.//4.4e-110:553:96//AF091081

R-HEMBA1004276

R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//1.9e-106:538:97//AF022795

R-HEMBA1004289//RPCI11-74010.TJ RPCI11 Homo sapiens genomic clone R-74010, genomic survey sequence.//2.3e-37:248:76//AQ266668

R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end.//0.0016:273:64//L13174

R-HEMBA1004306//HS_3175_B2_F01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence.//1.6e-28:190:77//AQ169206

R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence.//
6.3e-36:267:82//AC003088

R-HEMBA1004321//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 101
55, WORKING DRAFT SEQUENCE.//4.1e-111:576:95//AJ009611

R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 237
4C8, genomic survey sequence.//2.7e-42:136:91//AQ114933

R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic clone 23
03L24, genomic survey sequence.//1.0:78:67//AQ017600

R-HEMBA1004330//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5
unordered pieces.//2.3e-119:580:98//AC004987

R-HEMBA1004334//Pimpinella brachycarpa Phyb1 mRNA, complete cds.//3.3e-1
4:238:69//AF082024

R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10,
complete sequence.//1.8e-21:291:71//AC004638

R-HEMBA1004341

R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cd
s.//4.1e-74:444:90//D89667

R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmid
s R29515 and R28253, genomic sequence, complete sequence.//7.0e-38:287:8
2//AC003002

R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:92//I58
611

R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-14:446
:63//AC005949

R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic clone 20
05C13, genomic survey sequence.//0.010:334:61//B55811

R-HEMBA1004389//Homo sapiens full length insert cDNA clone ZE09A11.//1.5
e-19:170:83//AF086540

R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repeat.//1

.0:50:84//X58124

R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:69//AC004057

R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//AC005030

R-HEMBA1004408

R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200

R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-32:460:68//AJ011930

R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.9e-113:581:96//AC004846

R-HEMBA1004461//HS_3244_A2_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876

R-HEMBA1004479//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-40:485:70//AC006012

R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:513:59//AE001370

R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.//2.0e-08:245:66//AC005951

R-HEMBA1004506//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487

R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266

R-HEMBA1004509

R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230

R-HEMBA1004538//HS_3189_B2_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330

R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey sequence.//1.7e-16:116:93//B73329

R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457

R-HEMBA1004573

R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:60//Z68279

R-HEMBA1004586

R-nnnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551

R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62//AL022071

R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501.//1.4e-50:327:85//AB007970

R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//4.4e-13:527:63//AC004805

R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//U31866

R-HEMBA1004632

R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-117:573:98//AC005534

R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076

R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence.//0.00013:501:58//AC005171

R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete

sequence.//1.5e-120:571:98//AL031432

R-HEMBA1004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//4.4e-12:110:88//Z93241

R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//Z99291

R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MP012, complete sequence.//0.86:309:57//AB006702

R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic survey sequence.//0.29:331:61//B97342

R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559

R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-49:497:76//AC004638

R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//1.6e-38:362:79//AC005562

R-HEMBA1004725

R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:79//AC002085

R-HEMBA1004733

R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island, ESTs, STS, and GSSs, complete sequence.//0.0030:362:61//AL022395

R-HEMBA1004736//Homo sapiens clone DJ0981007, complete sequence.//1.9e-58:282:87//AC006017

R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:81//AC004953

R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STS

s and a polymorphic CA repeat.//5.3e-40:266:89//Z98950

R-HEMBA1004752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING DRAFT SEQUENCE.//3.3e-39:281:85//AL031121

R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//L06498

R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6 p21.31-22.1. Contains histone genes H2A/1,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island.//1.8e-08:516:59//AL021807

R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:72//AC004057

R-HEMBA1004763

R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310

R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:476:61//AE001371

R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete sequence.//5.0e-08:113:80//AC003047

R-HEMBA1004776

R-HEMBA1004778//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567

R-nnnnnnnnnnnnn//HS_3192_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855

R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:

318:87//AF048728

R-HEMBA1004806

R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-20:333:69//AC005015

R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545

R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002

R-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//7.6e-80:297:85//X53744

R-HEMBA1004850

R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201

R-HEMBA1004864

R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPCI11-46604 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297

R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-49:551:73//AC004826

R-HEMBA1004889//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943

R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//6.6e-11:144:77//AC005972

R-HEMBA1004909//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052

R-HEMBA1004918//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554

R-HEMBA1004923//Homo sapiens 47kB DNA fragment from Xq28, proximal to MT M1 gene.//2.0e-07:182:69//Y15994

R-HEMBA1004929

R-HEMBA1004930//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.7e-66:547:79//AC005848

R-HEMBA1004933//H.sapiens Humig mRNA.//0.13:233:62//X72755

R-HEMBA1004934//CIT-HSP-2021I16.TF CIT-HSP Homo sapiens genomic clone 2021I16, genomic survey sequence.//0.66:268:62//B65345

R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849

R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146_P_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00082:385:60//AC005341

R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408

R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249

R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982

R-HEMBA1004973//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.69:179:64//AC003656

R-HEMBA1004977//Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495

R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3

(Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSS and GSSs, complete sequence.//0.20:427:60//AL024509

R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614

R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389

R-HEMBA1004995//Homo sapiens chromosome 16, cosmid clone 306E5 (LANL), complete sequence.//1.6e-90:527:89//AC004224

R-HEMBA1005008//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663

R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474

R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548

R-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSS, GSSs and genomic marker D6S464, complete sequence.//3.1e-67:493:83//AL009179

R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//7.4e-101:537:94//AC004596

R-HEMBA1005039//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650

R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819

R-HEMBA1005050//Human Chromosome X PAC RPC11-290C9 from the Pieter de Jong Human PAC library; complete sequence.//4.0e-43:371:80//AC002404

R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//2.3e-15:269:66//AC004675

R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-30:305:74//AC006030

R-HEMBA1005075

R-HEMBA1005079//Homo sapiens clone HS19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156

R-HEMBA1005083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.3e-15:142:83//AL034423

R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//5.3e-110:545:96//AF080561

R-HEMBA1005113//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS ** * from clone Y53C10, WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340

R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//7.1e-55:306:82//AL022336

R-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//6.4e-45:309:87//AL022345

R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds.//3.2e-31:310:76//U81834

R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6 p22.3-23. Contains CpG island.//1.4e-33:361:79//AL021407

R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35. 1-36.13 Contains CA repeat, STS, complete sequence.//2.7e-22:440:66//AL031279

R-HEMBA1005185//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.0017:381:58//AL022594

R-HEMBA1005201//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.5e-05:457:57//X95276

R-HEMBA1005202//Human 18S ribosomal RNA.//4.7e-38:236:91//X03205

R-HEMBA1005219

R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//1.0:209:65//AC004854

R-HEMBA1005232//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0040:439:58//AC004617

R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//4.2e-111:568:96//AC005154

R-HEMBA1005244//HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence.//4.9e-12:116:84//AQ127947

R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//3.2e-27:210:84//AC004548

R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//4.6e-105:437:97//AC005837

R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system.//0.011:339:59//D86630

R-HEMBA1005275//Homo sapiens PAC clone DJ0886008 from 7q32-q35, complete sequence.//3.4e-17:269:71//AC004914

R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chr

osome 13q12-13 contains xs7 mRNA, ESTs.//6.9e-20:193:73//Z75887
R-HEMBA1005296//HS_3037_B1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence.//0.26:184:64//AQ117120
R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-58:445:78//AC006146
R-HEMBA1005311//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796E4, WORKING DRAFT SEQUENCE.//9.3e-42:383:78//AL022337
R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11.//0.80:179:65//AF003389
R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-40:409:71//AC006030
R-HEMBA1005318//S.pombe chromosome I cosmid c2E11.//0.97:370:61//AL031181
R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence.//1.9e-112:577:95//AC005803
R-HEMBA1005353//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 429E7, WORKING DRAFT SEQUENCE.//8.9e-80:406:97//AL031722
R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-50:320:84//AC005412
R-HEMBA1005367//RPC111-85E23.TV RPC111 Homo sapiens genomic clone R-85E23, genomic survey sequence.//0.39:148:67//AQ281915
R-HEMBA1005372//Homo sapiens full length insert cDNA YH93B03.//2.6e-108:557:95//AF074997
R-HEMBA1005374//Homo sapiens full length insert cDNA clone ZA95D11.//1.9e-110:531:98//AF086142
R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tpx3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROT

EIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//6.0e-41:432:75//Z92542

R-HEMBA1005394//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE.//4.9e-107:585:93//AL031670

R-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//5.1e-118:586:97//AL034379

R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06:204:68//U95958

R-HEMBA1005410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722

R-HEMBA1005411//RPCI11-66N19.TK RPCI11 Homo sapiens genomic clone R-66N19, genomic survey sequence.//2.2e-38:222:79//AQ237442

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//5.6e-117:453:99//AF041248

R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//0.86:278:60//Z97196

R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391

R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054

R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//4.0e-27:469:66//AC004894

R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//7.2e-40:410:76//AC005212

R-HEMBA1005472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524

R-HEMBA1005475//HS_2266_B2_C04_MF CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:209:61//AQ069377

R-HEMBA1005497

R-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence.//4.5e-116:580:97//AC004957

R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826

R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:59//AF003509

R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.44:195:63//Z96811

R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcript on control protein (BICP4) gene, complete cds.//0.44:470:57//L14320

R-HEMBA1005518//M.musculus mRNA for paladin gene.//6.2e-29:183:81//X99384

R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-40:281:86//AC004913

R-HEMBA1005526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//3.9e-40:482:73//Z97985

R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//3.8e-84:309:99//AB020860

R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence.//8.1e-25:154:94//U84091

R-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING DRAFT SEQUENCE.//5.3e-105:534:96//AL034431

R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//2.8e-69:432:88//AC004743

R-HEMBA1005558

R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087

R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.2-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//2.2e-67:399:91//AL020989

R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence.//1.0:156:63//AC005737

R-HEMBA1005577

R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds.//9.7e-27:561:64//AB011538

R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 -cytochrome oxidase 2 genes.//2.3e-10:404:62//X02171

R-HEMBA1005583//HS_3014_B1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence.//3.0e-81:442:94//AQ154499

R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSS and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046

R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//2.2e-28:262:79//AC005746

R-HEMBA1005595//HS_2224_A2_G03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence.//3.6e-48:263:95//AQ033446

R-HEMBA1005606//Human PAC clone DJ0093I03 from Xq23, complete sequence.//2.5e-08:355:63//AC003983

R-HEMBA1005609//HS_2182_B1_H06_MF CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130

R-HEMBA1005616//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176

R-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731

R-HEMBA1005627//Homo sapiens full length insert cDNA clone ZD53D02.//4.5e-72:398:93//AF086321

R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460

R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.4e-13:172:75//AL022069

R-HEMBA1005634//RPCI11-13015.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-13015, genomic survey sequence.//1.0e-28:153:82//B73293

R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786

R-HEMBA1005670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995

R-HEMBA1005679//Human esterase D mRNA, 3' end.//4.2e-49:322:88//M13450

R-HEMBA1005680//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC0059

24

R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds.//5.4e-46:376:84//U66406

R-HEMBA1005705//RPCI11-13014.TP RPCI-11 Homo sapiens genomic clone RPCI-

11-13014, genomic survey sequence.//0.071:182:59//B76186

R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.0:189:66//Z92545

R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces.//2.1e-47:449:75//AC003023

R-HEMBA1005737

R-nnnnnnnnnnnnn//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255

R-HEMBA1005755//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//0.15:160:65//AL008634

R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence.//5.2e-39:422:74//U71148

R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.037:261:61//AP000010

R-HEMBA1005813//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.7e-26:242:80//AL023808

R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds.//0.17:199:62//U52805

R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence.//0.26:437:56//AL034559

R-HEMBA1005829//Human Cosmid g1572c035, complete sequence.//3.8e-05:366:61//AC000124

R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs

, complete sequence.//8.2e-107:551:96//AL031781
R-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aA4, genomic survey
sequence.//2.6e-17:225:72//AL018730
R-HEMBA1005853//Human Chromosome 15 pac pDJ24m8, complete sequence.//1.1
e-27:314:75//AC000379
R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Canc
er Institute Human BAC Library) complete sequence.//2.6e-20:328:67//AC00
6207
R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, com
plete sequence.//2.0e-102:543:95//AC004945
R-HEMBA1005894
R-HEMBA1005909
R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 234
2E5, genomic survey sequence.//0.0012:315:60//AQ058081
R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn
, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6.//0.0090:445:58//Z2
3072
R-HEMBA1005931//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 54B20, WORKING DRAFT SEQUENCE.//1.7e-46:351:83//Z98304
R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261_A_13, complet
e sequence.//0.0052:179:71//AC005138
R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence.//1.1e-11
:149:74//AC005045
R-HEMBA1005963//HS_3055_A1_E08_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey
sequence.//5.4e-79:403:97//AQ147357
R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, comple
te cds.//6.9e-112:580:95//AF082516
R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1q24.1-

24.3. Contains STSs, GSSs, genomic marker D1S210 and a ca repeat polymorphism, complete sequence.//2.6e-39:299:82//AL031285

R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds.//6.3e-15:174:78//AF056035

R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//2.6e-112:574:95//AF036405

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds.//7.6e-27:444:67//AB018268

R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.025:373:60//AC005139

R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//0.0056:535:59//AC004125

R-HEMBA1006042//HS_2169_A1_B11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2169 Col=21 Row=C, genomic survey sequence.//1.7e-73:390:95//AQ132995

R-nnnnnnnnnnnnn

R-HEMBA1006081

R-HEMBA1006090//HS_2262_A2_A01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=2 Row=A, genomic survey sequence.//2.1e-70:360:97//AQ216324

R-HEMBA1006091

R-HEMBA1006100//Homo sapiens DNA sequence from PAC 212G6 on chromosome X p11.3-p11.4. Contains synapsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.//1.6e-36:354:77//AL009172

R-HEMBA1006108

R-HEMBA1006121

R-HEMBA1006124//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-
qter. Contains ESTs, STSs and polymorphic CA repeat.//1.3e-12:327:64//Z9
5113

R-HEMBA1006130//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62
//AC005948

R-nnnnnnnnnnnnn//Homo sapiens chromosome 19, cosmid F16403, complete sequ
ence.//4.3e-52:321:80//AC005777

R-HEMBA1006142//, complete sequence.//1.0e-13:160:78//AC005500

R-HEMBA1006155//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic
sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389:60//AC
004688

R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7
) gene, complete cds.//1.4e-119:574:98//AF048693

R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, c
omplete cds.//4.1e-43:307:86//U28217

R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete
sequence.//1.7e-30:300:71//AC004491

R-HEMBA1006198//***ALU WARNING: Human Alu-J subfamily consensus sequence
.//1.3e-36:284:85//U14567

R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97
//AF070557

R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.
46:365:58//AB014567

R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete
sequence.//2.8e-41:438:71//U91323

R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds.//
1.8e-28:179:91//AF083384

R-HEMBA1006259//RPCI11-44N14.TJ RPCI11 Homo sapiens genomic clone R-44N1

4, genomic survey sequence.//1.5e-48:348:85//AQ203161
R-HEMBA1006268
R-HEMBA1006272//Human DNA sequence from clone 1198H6 on chromosome 1p36.
11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME L
IKE genes. Contains GSSs and ESTs, complete sequence.//2.8e-73:273:87//A
L023753
R-nnnnnnnnnnnnn//H.sapiens PAP mRNA.//1.6e-54:585:71//X76770
R-HEMBA1006283//Sequence 7 from patent US 5776683.//9.7e-18:113:98//AR01
6240
R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028_K_7, complet
e sequence.//0.97:447:59//AC004585
R-HEMBA1006291//Homo sapiens full length insert cDNA clone ZB76B10.//2.9
e-94:454:98//AF086161
R-HEMBA1006293//Sequence 8 from patent US 5721351.//8.1e-10:111:72//I894
15
R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING
DRAFT SEQUENCE, 2 ordered pieces.//8.6e-37:288:84//AC005412
R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PAC
S-1) mRNA, complete cds.//6.5e-29:132:81//AF076183
R-HEMBA1006328//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 894K16, WORKING DRAFT SEQUENCE.//3.3e-50:340:75//AL034429
R-HEMBA1006334
R-HEMBA1006344//Rattus norvegicus nitzin mRNA, partial cds.//8.7e-22:259
:72//AF087945
R-HEMBA1006347//Human prostatic gene, complete cds.//1.8e-78:170:100//U3
3446
R-HEMBA1006349//Rat brain calcium channel alpha-1 subunit mRNA, complete
cds.//0.00051:120:73//M57682
R-HEMBA1006359//CITBI-E1-2516C16.TR CITBI-E1 Homo sapiens genomic clone

2516C16, genomic survey sequence.//4.7e-74:576:82//AQ277951
R-HEMBA1006364//G.gallus gene for transforming growth factor-beta2, exon
s 5-7.//2.5e-21:118:85//X59080
R-HEMBA1006377//Homo sapiens chromosome 19, cosmid F23149, complete sequ
ence.//5.7e-68:367:85//AC005239
R-HEMBA1006380//Human BAC clone RG007J15 from 7q31, complete sequence.//
6.1e-47:300:83//AC003989
R-HEMBA1006381//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), co
mplete sequence.//1.5e-47:336:86//AC005914
R-HEMBA1006398//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155),
complete sequence.//1.5e-67:501:83//AC005609
R-HEMBA1006416//Homo sapiens chromosome 17, clone 347_H_5, complete sequ
ence.//4.4e-37:319:76//AC002119
R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, complete s
equence.//2.9e-50:502:75//AC004253
R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transfor
ming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown g
enes.//4.1e-116:572:97//AF107885
R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-2
7. Contains the 3' part of the alternatively spliced gene for the human
orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and
zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSS and GSSs
, complete sequence.//9.4e-117:578:97//AL031781
R-HEMBA1006426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 291J10, WORKING DRAFT SEQUENCE.//2.2e-08:353:63//Z93017
R-HEMBA1006438//HS_2008_A1_D04_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, genomic survey s
equence.//1.2e-29:194:91//AQ245162
R-HEMBA1006445//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 u

nordered pieces.//0.011:330:60//AC005075

R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.032:256:61//AE001398

R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//5.6e-35:229:77//AC002364

R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, complete sequence.//1.1e-14:354:63//AC002052

R-HEMBA1006471

R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of 3].//1.1e-14:442:60//S67502

R-HEMBA1006483//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//3.7e-37:290:82//U95742

R-HEMBA1006485//H.sapiens mRNA for aminopeptidase.//7.6e-91:517:91//Y07701

R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-33:289:81//AC005089

R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//6.0e-07:485:60//AL020989

R-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//4.3e-112:572:95//AC005828

R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.3e-10:186:67//AC002994

R-HEMBA1006497//RPCI11-16L10.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16L10, genomic survey sequence.//1.5e-10:75:100//B88015

R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein

gene. Contains STSS, GSSs and a CA repeat polymorphism, complete sequence.//3.3e-36:516:70//Z93929

R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//1.2e-115:570:96//AB014566

R-HEMBA1006521//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//2.2e-20:266:71//Z98304

R-HEMBA1006530//RPCI11-52M1.TJ RPCI11 Homo sapiens genomic clone R-52M1, genomic survey sequence.//0.00015:227:64//AQ052526

R-HEMBA1006535//HS_2234_B1_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence.//7.5e-33:191:95//AQ129525

R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence.//0.026:497:58//AC005007

R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence.//5.2e-41:289:86//AC004603

R-HEMBA1006559//Mus musculus PRAJA1 (Praj1) mRNA, complete cds.//3.4e-64:551:78//U06944

R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//5.7e-09:266:66//AC002554

R-HEMBA1006566//HS_2171_B1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence.//0.012:306:61//AQ125421

R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//3.8e-70:529:82//U39357

R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete sequence.//1.0:141:65//AC006032

R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ111875

R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic

c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//A
C004709

R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-45:371:80//AC005031

R-HEMBA1006612

R-HEMBA1006617//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 8B22, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737

R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284

R-HEMBA1006631//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848

R-HEMBA1006635//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572

R-HEMBA1006639

R-HEMBA1006643

R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282

R-HEMBA1006652//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//8.7e-54:334:76//AC002089

R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390

R-HEMBA1006665//HS_3213_B2_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625

R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9

QTEL00023.seq.//2.6e-32:212:83//Z96776
R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551
R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608
R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096
R-HEMBA1006696
R-HEMBA1006708
R-HEMBA1006709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 715N11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674
R-HEMBA1006717
R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//9.9e-18:365:66//AC005828
R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327024, complete sequence.//1.3e-37:380:75//AC003108
R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H87), complete sequence.//2.1e-75:338:85//AC003951
R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//1.2e-112:579:95//AC005752
R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551
R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//2.3e-46:305:87//AC005701
R-HEMBA1006780//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSS and GSSs, complete sequence.//7.2e-39:305:82//AL022323
R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61//AL031317

R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//4.1e-43:355:80//AC006120

R-HEMBA1006796//HS_3038_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, genomic survey sequence.//0.99:158:63//AQ102483

R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//8.4e-47:481:75//AC004854

R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62_0_9, complete sequence.//3.0e-08:84:90//AC004797

R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromosome X p22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:496:76//Z93023

R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243_K_12, complete sequence.//0.70:206:65//AC005668

R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-46:281:91//AC004217

R-HEMBA1006865//Mus musculus clone 101.B1 repeat region sequence.//0.61:115:70//AF056074

R-nnnnnnnnnnnnn//Mus musculus mRNA for oxysterol-binding protein, complete cds.//3.3e-102:618:87//AB017026

R-HEMBA1006885

4.2e-14:379:63//AG006839

R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395

R-HEMBA1006921//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.1e-68:267:86//AC005154

R-HEMBA1006926

R-HEMBA1006929//HS_3244_A2_C01_T7 CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, genomic survey sequence.//6.9e-21:191:83//AQ207500

R-HEMBA1006936

R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853

R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//2.0e-75:371:98//AJ010841

R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, complete sequence.//0.47:240:63//AC005518

R-HEMBA1006973//HS_2009_A2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, genomic survey sequence.//9.6e-05:407:60//AQ232302

R-HEMBA1006976//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701

R-HEMBA1006993//Human thymopoietin (TMP0) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.9e-47:394:79//U18271

R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic clone 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406

R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558

R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//5.6e-41:437:71//AC005277

R-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//8.2e-73:556:80//X79088

R-HEMBA1007045

R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11

.2-qter contains EST.//9.9e-27:342:71//Z72006
R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region
./5.4e-85:558:87//U85056
R-HEMBA1007062
R-HEMBA1007066
R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421_E_14, complete
sequence.//2.0e-66:476:85//AC006141
R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60_A_24, complete
sequence.//1.0e-38:179:82//AC005325
R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6
unordered pieces.//3.2e-49:551:73//AC006015
R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequence.//1
.0:261:61//AC000385
R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE,
37 unordered pieces.//0.043:295:62//AC004803
R-HEMBA1007113//Homo sapiens (subclone 6_a8 from P1 H16) DNA sequence.//
1.4e-52:307:87//L43392
R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Cont
ains STS.//1.2e-08:131:75//Z92547
R-HEMBA1007147//H.sapiens CpG island DNA genomic MseI fragment, clone 65
f1, reverse read cpg65f1.rtl1a.//0.16:187:64//Z62246
R-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequ
ence.//7.6e-108:543:96//AC005239
R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 from 7q31, complete seq
uence.//0.14:323:58//AC004875
R-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-103:529:
94//AF062085
R-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORK
ING DRAFT SEQUENCE, 129 ordered pieces.//5.4e-106:537:96//AC005911

R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.1e-39:262:80//AC003035

R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.3e-61:332:95//D86987

R-HEMBA1007206//Homo sapiens DNA sequence from PAC 958B3 on chromosome X p22.11-Xp22.22. Contains ESTs STS and CpG island.//1.9e-50:436:81//Z93023

R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.3e-96:471:97//AB018340

R-HEMBA1007251//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//0.011:349:62//AC004777

R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 from 7q35-q36, complete sequence.//2.8e-10:224:70//AC004856

R-HEMBA1007267//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.4e-53:362:86//AC005924

R-HEMBA1007273

R-HEMBA1007279//Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4.//0.042:454:57//AJ235273

R-HEMBA1007281//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.99:288:60//AJ235272

R-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//7.4e-107:554:95//AL031003

R-HEMBA1007300//Caenorhabditis elegans cosmid C48C5.//0.22:474:59//U39994

R-HEMBA1007301

R-HEMBA1007319//Campylobacter jejuni repetitive DNA, clone pINT.//4.9e-0

8:524:58//Y14425

R-HEMBA1007320//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14 /28, WORKING DRAFT SEQUENCE.//3.4e-16:244:71//AP000043

R-HEMBA1007322//Homo sapiens BAC clone RG324D18 from 7p15-p21, complete sequence.//3.9e-83:383:85//AC005251

R-HEMBA1007327//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c lone 7706, WORKING DRAFT SEQUENCE.//1.6e-38:533:71//Z96804

R-HEMBA1007341//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c lone 268D13, WORKING DRAFT SEQUENCE.//3.6e-21:394:66//AL023513

R-HEMBA1007342//Human BAC clone GS368F15 from 7q31, complete sequence.// 1.7e-15:190:73//AC003080

R-HEMBA1007347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c lone N38G6, WORKING DRAFT SEQUENCE.//2.2e-47:455:77//Z96802

R-HEMBB1000005//Homo sapiens 3p21.1-9 PAC RPCI4-793P23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-62:539:79//AC0 06208

R-HEMBB1000008//Homo sapiens chromosome 17, clone hCIT.211_P_7, complete sequence.//1.2e-36:285:83//AC003665

R-HEMBB1000018//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-51:416:79//AC004820

R-HEMBB1000024//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSS and polymorphic CA repeat.//3.9e-18:211:79//Z9 5113

R-HEMBB1000025//HS_3064_B2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=14 Row=D, genomic survey sequence.//5.9e-40:254:90//AQ132765

R-HEMBB1000030//Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS, complete sequence.//1

.5e-32:452:70//Z85986

R-HEM BB1000036//CIT-HSP-2024L15.TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey sequence.//9.3e-63:541:77//B66264

R-HEM BB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//7.6e-91:467:97//AF084928

R-HEM BB1000039//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//2.4e-44:456:68//AC005291

R-HEM BB1000044//Human BAC clone RG016J04 from 7q21, complete sequence.//1.4e-54:307:80//AC002064

R-HEM BB1000048//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//3.8e-09:330:63//AC002300

R-HEM BB1000050//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RSL gene for retinoschisis (X-linked, juvenile) 1 (XLRSL). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056

R-HEM BB1000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521

R-HEM BB1000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806

R-HEM BB1000059//Homo sapiens clone DJ0850I01, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC006009

R-HEM BB1000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840

R-HEM BB1000089//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520

R-HEM BB1000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein an

d the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715

R-HEMBB1000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115

R-HEMBB1000113//HS_3013_A1_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730

R-HEMBB1000119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521

R-HEMBB1000136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407

R-HEMBB1000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945

R-HEMBB1000144//Homo sapiens chromosome 17, clone hCIT.507_E_2, complete sequence.//0.00083:206:66//AC004134

R-HEMBB1000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085

R-HEMBB1000175

R-HEMBB1000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368

R-HEMBB1000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.

6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397

R-HEM BB1000217

R-HEM BB1000218//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216

R-HEM BB1000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706

R-HEM BB1000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308

R-HEM BB1000244//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420

R-HEM BB1000250//Human DNA sequence from clone 34B20 on chromosome 6p21.3 1-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777

R-HEM BB1000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328

R-HEM BB1000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765

R-HEM BB1000266//RPCI11-76C20.TV RPCI11 Homo sapiens genomic clone R-76C20, genomic survey sequence.//1.0:232:59//AQ265533

R-HEM BB1000272//HS_3032_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence.//0.0082:209:62//AQ096702

R-HEM BB1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGL

C Region, complete sequence.//1.6e-45:277:72//AC000053

R-HEM BB1000284//Homo sapiens full length insert cDNA clone YY88A05.//6.9e-112:572:96//AF088018

R-HEM BB1000307//Homo sapiens chromosome 17, clone hRPK.471_L_13, complete sequence.//5.7e-96:523:93//AC005244

R-HEM BB1000312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//7.5e-21:218:67//AL023693

R-HEM BB1000317//Toxoplasma gondii chloroplast, complete genome.//0.062:354:58//U87145

R-HEM BB1000318//Human DNA sequence from PAC 292H14 on chromosome Xp21. Contains STS and CA repeat polymorphism.//4.5e-52:302:81//AL008710

R-HEM BB1000335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//1.9e-16:139:84//AC005179

R-HEM BB1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//0.0062:231:64//AJ003147

R-HEM BB1000337//CIT-HSP-2329010.TF CIT-HSP Homo sapiens genomic clone 2329010, genomic survey sequence.//1.2e-31:192:92//AQ035976

R-HEM BB1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//1.9e-39:477:71//AC004605

R-HEM BB1000339//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//4.1e-54:357:76//AL031681

R-HEM BB1000341//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.8e-19:501:63//AC002350

R-HEM BB1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence.//3.6e-41:457:72//AC004644

R-HEM BB1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene

e RNA binding protein, ESTs, GSS.//7.2e-36:325:74//Z98751
R-HEMBB1000369//Homo sapiens chromosome 4 clone B366024 map 4q25, complete sequence.//9.0e-25:179:79//AC004067
R-HEMBB1000374//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 75N14, WORKING DRAFT SEQUENCE.//8.4e-58:332:79//Z97199
R-HEMBB1000376//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.1e-47:309:88//D87675
R-HEMBB1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-46:302:85//AC005080
R-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//1.0e-107:531:97//AF076838
R-HEMBB1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//1.1e-25:441:67//Z98052
R-HEMBB1000404//HS_2246_A2_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence.//0.0025:196:63//AQ084251
R-HEMBB1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGL C Region, complete sequence.//1.2e-29:358:72//AC000053
R-HEMBB1000434//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.8e-51:299:89//AC004069
R-HEMBB1000438//HS_2239_B2_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence.//1.3e-10:76:100//AQ067700
R-HEMBB1000441//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//4.4e-60:281:90//Z82207
R-HEMBB1000449//Homo sapiens clone DJ0898018, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.8e-11:228:68//AC004920
R-HEMBB1000455//Homo sapiens clone GS051M12, complete sequence.//3.1e-14

:388:65//AC005007

R-HEMBB1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//4.9e-34:320:79//AC003104

R-HEMBB1000480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//3.4e-36:285:82//Z83849.

R-HEMBB1000487

R-HEMBB1000490//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.5e-34:281:81//AL034423

R-HEMBB1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//8.5e-37:483:72//Z93023

R-HEMBB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721

R-HEMBB1000510//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//7.1e-44:221:80//AL033397

R-HEMBB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//3.5e-51:280:90//AC002477

R-HEMBB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//1.7e-53:304:82//AC004079

R-HEMBB1000530//Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.//4.2e-74:428:92//AC006236

R-HEMBB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete

sequence.//5.6e-13:112:80//U91321

R-HEM BB1000554//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 409J21, WORKING DRAFT SEQUENCE.//5.1e-14:239:63//Z83824

R-HEM BB1000556//Homo sapiens envoplakin (EVPL) mRNA, complete cds.//0.03
1:275:60//U53786

R-HEM BB1000564//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), co
mplete sequence.//3.1e-17:227:76//AC005914

R-HEM BB1000573//Borrelia afzelii (strain NT28) DNA, internal transcribed
spacer.//0.078:161:63//D84405

R-HEM BB1000575//Homo sapiens chromosome 17, clone hRPC.859_0_20, complet
e sequence.//7.2e-52:260:80//AC003695

R-HEM BB1000586//Human DNA sequence from cosmid V210E9, between markers D
XS366 and DXS87 on chromosome X.//2.0e-33:305:79//Z70280

R-HEM BB1000589//Homo sapiens chromosome 17, clone hRPK.1064_E_11, comple
te sequence.//1.3e-14:409:65//AC005208

R-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Sys
tems Human BAC Library) complete sequence.//6.2e-39:493:71//AC005184

R-HEM BB1000592//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Can
cer Institute Human PAC Library) complete sequence.//1.6e-08:254:64//AC0
05831

R-HEM BB1000598//Homo sapiens chromosome 11 pac pDJ159o1, complete sequen
ce.//3.3e-38:407:76//AC000381

R-HEM BB1000623//CIT-HSP-2374P17.TR CIT-HSP Homo sapiens genomic clone 23
74P17, genomic survey sequence.//1.3e-41:212:100//AQ109717

R-HEM BB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3
-24.3. Contains a hamster Androgen-dependent Expressed Protein like prot
ein gene, ESTs and GSSs, complete sequence.//5.2e-31:319:78//AL022724

R-HEM BB1000631//Sequence 28 from patent US 5708157.//6.8e-20:208:80//I80
058

R-HEMBB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.4e-47:457:75//AC004176

R-HEMBB1000637//Human BAC clone RG094H21 from 7q21-q22, complete sequence.//2.9e-45:263:87//AC003085

R-HEMBB1000638//Genomic sequence from Human 6, complete sequence.//9.1e-34:375:73//AC002112

R-HEMBB1000643//HS_2242_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence.//0.010:239:60//AQ065993

R-HEMBB1000649//Homo sapiens RBP56/hTAFII68 gene, exon 7.//8.3e-63:306:100//AB010061

R-HEMBB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMPR (GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic CA repeat.//3.3e-14:450:64//AL009031

R-HEMBB1000665//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MXA21, complete sequence.//0.98:251:63//AB005247

R-HEMBB1000671//Human DNA sequence from PAC 106C24, between markers DXS294 and DXS730 on chromosome X.//6.8e-58:296:85//Z83313

R-HEMBB1000673//CITBI-E1-2506F20.TR CITBI-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731

R-HEMBB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584

R-nnnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds.//2.0e-50:287:93//AF040723

R-HEMBB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943

R-HEM BB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380

R-HEM BB1000709//RPCI11-79A8.TV RPCI11 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374

R-HEM BB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MGN6, complete sequence.//0.00018:386:60//AB017066

R-HEM BB1000726//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990

R-HEM BB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875

R-HEM BB1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069

R-HEM BB1000763//Plasmid Col Ib-P9 (from E.coli K12) colicin Ib promoter region and 5' coding region.//1.0:115:63//K02071

R-HEM BB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205

R-HEM BB1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:154:67//AC003046

R-HEM BB1000789//RPCI11-2I14.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2I14, genomic survey sequence.//3.0e-09:299:64//B63628

R-HEM BB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:85//U95740

R-HEM BB1000794//HS_3253_A1_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291

R-HEM BB1000807

R-HEM BB1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542

R-HEM BB1000821

R-HEMBB1000822//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944

R-HEMBB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14 /28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043

R-HEMBB1000827//Homo sapiens clone DJ0981007, complete sequence.//6.8e-4 3:319:84//AC006017

R-HEMBB1000831//HS_3247_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850

R-HEMBB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6 . Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//4.2e-17:167:80//AL021368

R-HEMBB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283

R-HEMBB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086

R-HEMBB1000852//HS_3075_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816

R-HEMBB1000870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523

R-HEMBB1000876//Human DNA sequence from clone 91J24 on chromosome 6q24 C ontains part of utrophin Gene, part of cytochrome C oxidase gene, EST, C pG island, complete sequence.//0.0016:227:65//AL024474

R-HEMBB1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequ

ence.//0.62:238:62//AC005621

R-HEM BB1000887//Synthetic human/adenovirus type 5 recombination junction
 .//9.9e-24:275:76//M34061

R-HEM BB1000888//CIT-HSP-2282A13.TR CIT-HSP Homo sapiens genomic clone 22
 82A13, genomic survey sequence.//2.4e-05:310:60//AQ000826

R-HEM BB1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20
 unordered pieces.//6.5e-44:305:84//AC005995

R-HEM BB1000893//Homo sapiens BAC clone RG363E19 from 7q31.1, complete se
 quence.//3.7e-30:265:80//AC004492

R-HEM BB1000908//RPCI11-13P12.TV RPCI-11 Homo sapiens genomic clone RPCI-
 11-13P12, genomic survey sequence.//0.98:183:61//B76199

R-HEM BB1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IG
 LC Region, complete sequence.//1.7e-28:302:76//AC000024

R-HEM BB1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human
 BAC library) complete sequence.//4.1e-34:314:76//AC003037

R-HEM BB1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-224D6 co
 mplete sequence.//6.3e-09:536:59//U95739

R-HEM BB1000917//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
 lone 169I5, WORKING DRAFT SEQUENCE.//1.6e-47:234:86//Z93015

R-HEM BB1000927

R-HEM BB1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 22
 87M13, genomic survey sequence.//0.090:115:69//B99228

R-HEM BB1000959//Homo sapiens chromosome 17, clone HRPC905N1, complete se
 quence.//5.7e-89:544:90//AC003098

R-HEM BB1000973//Arabidopsis thaliana chromosome II BAC F2I9 genomic sequ
 ence, complete sequence.//0.038:377:58//AC005560

R-HEM BB1000975//Arabidopsis thaliana chromosome II BAC F5H14 genomic seq
 uence, complete sequence.//1.0e-05:342:62//AC006234

R-HEM BB1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone

2386J13, genomic survey sequence.//1.1e-18:231:74//AQ239443
R-HEM BB1000985//HS_3184_A1_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008
R-HEM BB1000991
R-HEM BB1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//1.4e-42:343:81//AC002368
R-HEM BB1001004
R-HEM BB1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence.//3.1e-57:317:94//AQ262056
R-HEM BB1001011//HS_3017_B1_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944
R-HEM BB1001014//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//2.4e-49:417:80//AL031662
R-HEM BB1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//7.6e-41:303:76//AC002549
R-HEM BB1001024//Homo sapiens (subclone 2_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475
R-HEM BB1001037//Homo sapiens 22q11 BAC Clone 489d1 In MDR Region, complete sequence.//2.0e-50:416:82//AC005527
R-HEM BB1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//AC004699
R-HEM BB1001051//H.sapiens mRNA for FAN protein.//7.1e-18:114:98//X96586
R-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.1e-94:520:93//AC006014
R-HEM BB1001058//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//1.1e-56:242:82//AC004187
R-HEM BB1001060//Human Tigger1 transposable element, complete consensus s

equence.//4.2e-66:323:81//U49973

R-HEM BB1001063//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 523G1, WORKING DRAFT SEQUENCE.//4.0e-114:556:98//AL034375

R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.8e-105:5
12:97//AF034803

R-HEM BB1001096//Human DNA sequence from PAC 24608, between markers DXS67
91 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735

R-HEM BB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-2
6.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related
, matrix associated, actin dependent regulator of chromatin, subfamily a
, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains
ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577

R-HEM BB1001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 462023, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431

R-HEM BB1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome
Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GT
R2-2), 5' UTR. ESTs, STS.//1.1e-38:306:84//Z99570

R-HEM BB1001117//RPCI11-35I8.TK RPCI-11 Homo sapiens genomic clone RPCI-1
1-35I8, genomic survey sequence.//1.5e-08:67:100//AQ047113

R-HEM BB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, compl
ete sequence.//9.0e-26:481:67//AC003071

R-HEM BB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 C
ontains STS, GSS, complete sequence.//0.045:127:69//Z99495

R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subuni
t mRNA, complete cds.//5.0e-23:285:73//M25077

R-HEM BB1001137//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from contig 4-09, complete sequence.//2.5e-07:334:62//AL010222

R-HEM BB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequenc
e.//2.5e-46:412:79//AC002564

R-HEM BB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA
./1.8e-11:148:77//U51904

R-HEM BB1001153//RPCI11-10L7.TP RPCI-11 Homo sapiens genomic clone RPCI-1
1-10L7, genomic survey sequence./2.3e-34:213:82//B71766

R-HEM BB1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete seq
uence./0.040:465:56//AC003070

R-nnnnnnnnnnnn//Sequence 1 from patent US 5618695./2.8e-15:176:80//I400
55

R-HEM BB1001177

R-HEM BB1001182//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from contig 4-52, complete sequence./1.9e-05:174:70//AL010226

R-HEM BB1001199

R-HEM BB1001208

R-HEM BB1001209//RPCI11-41E13.TP RPCI-11 Homo sapiens genomic clone RPCI-
11-41E13, genomic survey sequence./1.1e-95:473:97//AQ029098

R-HEM BB1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL),
complete sequence./6.2e-08:412:61//AC005199

R-HEM BB1001218//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-1
1-13L8, genomic survey sequence./1.0e-46:498:74//B75158

R-HEM BB1001221//RPCI11-62024.TJ RPCI11 Homo sapiens genomic clone R-6202
4, genomic survey sequence./3.2e-09:215:68//AQ200950

R-HEM BB1001234

R-HEM BB1001242

R-HEM BB1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4
unordered pieces./1.4e-33:361:72//AC005377

R-HEM BB1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene
cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseu
dogene, partial sequence./3.8e-105:517:98//AF042089

R-HEM BB1001254//Methanococcus jannaschii section 3 of 150 of the complet

e genome.//0.96:203:61//U67461

R-HEMBB1001267//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSS and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046

R-HEMBB1001271//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.//3.9e-47:494:75//AC005544

R-HEMBB1001282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184J9, WORKING DRAFT SEQUENCE.//0.0011:97:79//AL031428

R-HEMBB1001288

R-HEMBB1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//2.0e-31:301:78//AC005601

R-HEMBB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//0.053:283:60//AC003083

R-HEMBB1001302

R-HEMBB1001304//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//6.3e-15:396:64//AL033397

R-HEMBB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8SpN6, genomic survey sequence.//3.4e-42:293:86//AG013777

R-HEMBB1001315//Human NFE genomic fragment.//7.5e-30:243:78//M98511

R-HEMBB1001317//Homo sapiens chromosome 17, clone hRPC.1028_K_7, complete sequence.//2.3e-39:301:82//AC004585

R-HEMBB1001326//HS_3054_A1_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=K, genomic survey sequence.//0.90:117:63//AQ106096

R-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//0.037:103:77//D63850

R-HEMBB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//9.1e-19:229:77//AC003037

R-HEMBB1001337

R-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region .//2.9e-45:551:72//U85056

R-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.7e-59:292:99//AF097441

R-HEMBB1001348//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//9.1e-41:326:82//AC004859

R-HEMBB1001356//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//1.8e-11:213:67//Z82207

R-HEMBB1001364//HS_3050_A2_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=10 Row=K, genomic survey sequence.//1.8e-21:158:91//AQ133940

R-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p 11.2-10p12.1, complete sequence.//4.1e-37:419:73//AC005876

R-HEMBB1001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//9.5e-15:201:75//U91326

R-HEMBB1001369//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 477J10, WORKING DRAFT SEQUENCE.//1.8e-28:224:83//AL021686

R-HEMBB1001380//HS_2267_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2267 Col=21 Row=L, genomic survey sequence.//4.0e-14:100:95//AQ084896

R-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.6e-55:312:81//AF071314

R-HEMBB1001387//Homo sapiens chromosome 9, P1 clone 8660 (LBNL H105), complete sequence.//1.0:166:63//AC003953

R-HEMBB1001394//Homo sapiens chromosome 17, clone hRPK.215_E_13, complete

e sequence.//1.4e-55:494:76//AC005549

R-HEM BB1001410//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.011:208:63//AC006204

R-HEM BB1001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces.//1.5e-22:325:69//AC002370

R-HEM BB1001426//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-46:328:84//AC002350

R-HEM BB1001429//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.6e-105:550:95//AC006160

R-HEM BB1001436

R-HEM BB1001443//HS_2228_A1_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=9 Row=C, genomic survey sequence.//0.37:173:62//AQ066934

R-HEM BB1001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.7e-23:339:69//AC005522

R-HEM BB1001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.//1.1e-39:299:84//AC005355

R-HEM BB1001458//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//6.0e-05:486:59//AE001430

R-HEM BB1001463//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//1.2e-50:317:89//AC005154

R-HEM BB1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95:71//AQ107941

R-HEM BB1001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192:70//AF046762

R-HEM BB1001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu⁺⁺-transporting P-type ATPase exon

s 2 to 21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801
R-HEMBB1001521//Mus musculus clone OST1209, genomic survey sequence.//7.
5e-30:332:75//AF046642
R-HEMBB1001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 u
nordered pieces.//9.5e-55:483:76//AC005000
R-HEMBB1001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-
08:159:71//AC002070
R-HEMBB1001535//Human DNA sequence from cosmid E127C11 on chromosome 22q
11.2-qter contains STS.//4.0e-30:286:79//Z74581
R-HEMBB1001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete s
equence.//1.6e-39:342:80//U73169
R-HEMBB1001537//Genomic sequence from Human 9q34, complete sequence.//3.
7e-41:361:77//AC000394
R-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10,
complete sequence.//0.34:212:61//AC003049
R-HEMBB1001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, c
omplete sequence.//8.0e-40:267:88//AC002301
R-HEMBB1001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9
unordered pieces.//5.1e-30:286:76//AC005225
R-HEMBB1001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12
unordered pieces.//2.5e-15:194:75//AC004840
R-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.
22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234:79//AL0
31677
R-HEMBB1001586//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12
unordered pieces.//2.7e-30:371:74//AC005236
R-HEMBB1001588//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC lib
rary), complete sequence.//8.0e-32:323:73//AC003106
R-HEMBB1001603//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***

from contig 4-59, complete sequence.//0.034:302:59//AL010235

R-HEMBB1001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome X p22.11-Xp22.22. Contains ESTs STS and CpG island.//7.1e-31:503:68//Z9302

3

R-HEMBB1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing F MR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368

R-HEMBB1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228:82//Z86062

R-HEMBB1001635//Homo Sapiens Chromosome X clone bWDX90, complete sequence.//1.5e-23:407:69//AC004075

R-HEMBB1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing F MR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368

R-HEMBB1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSS, GSSs and genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506

R-HEMBB1001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344

R-HEMBB1001665//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572

R-HEMBB1001668

R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573:97//AB014546

R-HEMBB1001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//I86429

R-HEMBB1001685//Homo sapiens chromosome 17, clone hRPK.721_K_1, complete sequence.//2.6e-43:311:83//AC005411

R-HEMBB1001695

R-HEMBB1001704//CIT-HSP-2324C15.TR CIT-HSP Homo sapiens genomic clone 23

24C15, genomic survey sequence.//0.0074:259:58//AQ028704

R-HEMBB1001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.1e-34:296:80//AC004851

R-HEMBB1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020

R-HEMBB1001717//CIT-HSP-2378C19.TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992

R-HEMBB1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBNL H94), complete sequence.//1.8e-10:80:90//AC005613

R-HEMBB1001736//CIT-HSP-2369K6.TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221

R-HEMBB1001747//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA 1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671

R-HEMBB1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.4e-60:242:92//AC005829

R-HEMBB1001753//RPCI11-59J22.TK RPCI11 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046

R-HEMBB1001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130

R-HEMBB1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050

R-HEMBB1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157

R-HEMBB1001785//Torulopsis glabrata mitochondrial intergenic region ATPa

se 6 -ATPase 9 genes.//0.00073:189:65//X02170

R-HEM BB1001797//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140

R-HEM BB1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391

R-HEM BB1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882

R-HEM BB1001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996

R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCI P1) mRNA, complete cds.//1.7e-104:498:98//AF056209

R-HEM BB1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//AC005328

R-HEM BB1001839

R-HEM BB1001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MOP10, complete sequence.//0.00093:488:60//AB005241

R-HEM BB1001863//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436

R-HEM BB1001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327

R-HEM BB1001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MYN8, complete sequence.//0.26:303:59//AB020754

R-HEM BB1001869//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//7.0e-37:285:85//AC002553

R-HEM BB1001872//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS ** * from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//AL009027

R-HEM BB1001874

R-HEM BB1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.//0.037:406:60//AE001272

R-HEMBB1001880//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.//1.3e-49:461:77//AC005922

R-HEMBB1001899//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z98858

R-HEMBB1001905//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//1.9e-28:181:75//AL022345

R-HEMBB1001906

R-HEMBB1001908//Genomic sequence from Human 17, complete sequence.//2.9e-36:274:76//AC001231

R-HEMBB1001910//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//3.5e-41:408:76//AC003070

R-HEMBB1001911//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//6.1e-64:310:89//AJ011929

R-HEMBB1001915//Mouse mRNA for arylhydrocarbon receptor, complete cds.//2.0e-20:220:78//D38417

R-HEMBB1001921//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1141E15, WORKING DRAFT SEQUENCE.//1.9e-47:410:80//AL034422

R-HEMBB1001922//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//6.2e-32:378:74//AC004099

R-HEMBB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.2e-41:304:84//AC00406

R-HEMBB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 10/11 .//8.3e-12:202:69//AB020867

R-HEMBB1001944//P.falciparum gene for beta subunit RNA polymerase.//0.00090:264:62//X75544

R-HEMBB1001945//Swietenia humilis DNA for simple tandem repeat (242bp).//0.056:224:62//AJ000408

R-HEMBB1001947//RPCI11-60L13.TJ RPCI11 Homo sapiens genomic clone R-60L13, genomic survey sequence.//7.4e-23:146:94//AQ202335

R-HEMBB1001950//Human DNA sequence from clone 415G2 on chromosome 22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence.//0.57:115:68//Z83846

R-HEMBB1001952//Homo Sapiens Chromosome X clone bWXd171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-36:283:84//AC004676

R-HEMBB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.9e-60:334:82//AC005037

R-HEMBB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.9e-56:518:77//AC005077

R-HEMBB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//3.2e-19:157:86//AC005736

R-HEMBB1001967//Homo sapiens DNA for amyloid precursor protein, complete cds.//5.7e-68:314:89//D87675

R-HEMBB1001973//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE.//1.4e-37:484:70//AJ009617

R-HEMBB1001983//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//2.1e-28:286:75//AL034417

R-HEMBB1001988//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//6.9e-29:203:88//AL034420

R-HEMBB1001990//Homo sapiens full length insert cDNA clone ZC33G03.//7.8e-95:456:99//AF086192

R-HEMBB1001996

R-HEMBB1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENCE, 26 unordered pieces.//6.4e-26:162:83//AC005055

R-HEMBB1002002//Human DNA sequence from PAC 2A2 on chromosome X contains ESTs.//8.2e-83:362:93//Z84816

R-HEMBB1002005//Homo sapiens chromosome 3p clone RPCI5-1034C16, WORKING

DRAFT SEQUENCE, 45 unordered pieces.//8.5e-36:291:83//AC005903

R-HEMBB1002009//Homo sapiens clone DJ0828F13, complete sequence.//5.6e-08:307:65//AC004904

R-HEMBB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.9e-05:375:62//B36336

R-HEMBB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic clone 23 13E13, genomic survey sequence.//0.34:241:62//AQ028389

R-HEMBB1002043//Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence.//7.4e-35:297:82//AC005612

R-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.8e-96:582:90//AC005740

R-HEMBB1002045//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.7e-63:575:77//AC005778

R-HEMBB1002049//Human Chromosome X clone bWXD187, complete sequence.//1.9e-21:384:64//AC004383

R-HEMBB1002050//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//2.5e-37:368:76//AC005553

R-HEMBB1002068//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//0.30:167:65//AC004782

R-HEMBB1002069//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.3e-73:449:84//AC004799

R-HEMBB1002092//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//3.8e-45:307:87//AC005828

R-HEMBB1002094//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.1e-47:457:76//AC005943

R-HEMBB1002115//HS_2223_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2223 Col=19 Row=N, genomic survey sequence.//3.0e-58:295:98//AQ152279

R-HEMBB1002139//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.//6.6e-49:283:93//U14573

R-HEMBB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-45:451:76//AC006006

R-HEMBB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16 map 10 q25, complete sequence.//1.3e-57:359:81//AC005881

R-HEMBB1002189//Human Chromosome 11 pac pDJ392a17, complete sequence.//4.5e-43:420:77//AC000385

R-HEMBB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//8.2e-33:340:64//AC004913

R-HEMBB1002193//Sequence 5 from patent US 5709858.//3.2e-23:154:92//I80846

R-HEMBB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence.//2.6e-52:415:81//AF015148

R-HEMBB1002218//, complete sequence.//3.4e-17:178:82//AC005300

R-HEMBB1002232//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-55:292:88//AC004599

R-HEMBB1002247//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//2.9e-13:227:70//AC005829

R-HEMBB1002249//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//1.1e-06:284:64//AL031733

R-HEMBB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.3e-104:593:91//AC002415

R-HEMBB1002255//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//2.1e-40:284:85//Z93930

R-HEMBB1002266//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//1.3e-09:371:63//AL010216

R-HEMBB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, complete

sequence.//1.3e-39:247:86//AC004534
R-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.
//4.1e-84:549:86//U73642
R-HEMBB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete
sequence.//2.5e-10:164:71//AC004129
R-HEMBB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, complete
sequence.//0.39:365:59//AC005028
R-HEMBB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Library C
Homo sapiens genomic clone Plate=CT 771 Col=9 Row=H, genomic survey sequ
ence.//0.96:180:58//B39313
R-HEMBB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete
sequence.//7.9e-17:258:73//AC004849
R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.
//6.9e-96:479:97//AJ010841
R-HEMBB1002358//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics
) , PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5
(from Lawrence Livermore), complete sequence.//2.3e-53:309:83//AC002366
R-HEMBB1002359//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5
unordered pieces.//4.9e-27:350:74//AC005038
R-HEMBB1002364//Homo sapiens Xp22 PAC RPCI1-108M6 (Roswell Park Cancer C
enter PAC library) complete sequence.//8.6e-53:302:79//AC003036
R-HEMBB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapping to
chromosome 11, band p13.//3.2e-38:199:100//X04094
R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds.//3.2e-07:120:78//A
F072467
R-HEMBB1002383//Human DNA sequence from cosmid U19H10. on chromosome X. C
ontains ESTs and CA repeat.//0.98:351:58//AL021182
R-HEMBB1002387//HS-1052-B2-G10-MR.abi CIT Human Genomic Sperm Library C
Homo sapiens genomic clone Plate=CT 774 Col=20 Row=N, genomic survey seq

uence.//2.0e-07:276:67//B41091

R-HEMBB1002415//Homo sapiens chromosome 17, clone hRPK.209_D_14, complete sequence.//1.4e-25:202:79//AC005730

R-HEMBB1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//3.6e-60:401:87//AC004799

R-HEMBB1002442//Homo sapiens clone UWGC:r9a from 6p21, complete sequence.//3.1e-51:358:81//AC006046

R-HEMBB1002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING DRAFT SEQUENCE.//1.4e-115:557:98//AL034349

R-HEMBB1002457//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//6.3e-37:338:80//AL031012

R-HEMBB1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//9.7e-09:314:64//AE000659

R-HEMBB1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project).//0.42:110:74//AL021635

R-HEMBB1002489//Salvelinus fontinalis microsatellite sequence SFO-12.//6.6e-06:167:71//U50302

R-HEMBB1002492//RPCI11-74F21.TK RPCI11 Homo sapiens genomic clone R-74F21, genomic survey sequence.//3.1e-14:410:63//AQ238960

R-HEMBB1002495//HS_3220_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=14 Row=K, genomic survey sequence.//1.3e-24:137:100//AQ180762

R-HEMBB1002502//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//9.6e-81:538:86//AC006120

R-HEMBB1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.

//0.0061:482:57//AL031313

R-HEMBB1002510//HS_2179_A1_F03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=5 Row=K, genomic survey sequence.//6.9e-35:423:72//AQ298309

R-HEMBB1002520//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//2.0e-62:201:85//AL033397

R-HEMBB1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL H139), complete sequence.//0.99:323:58//AC004225

R-HEMBB1002531

R-HEMBB1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.0e-61:380:79//AP000009

R-HEMBB1002545//RPCI11-2F3.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2F3, genomic survey sequence.//3.5e-12:414:63//B63283

R-HEMBB1002550

R-HEMBB1002556//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.6e-62:299:85//AC006160

R-HEMBB1002579//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1141E15, WORKING DRAFT SEQUENCE.//1.7e-42:286:88//AL034422

R-HEMBB1002582//Homo sapiens clone DJ1119N05, complete sequence.//3.0e-14:426:60//AC004968

R-HEMBB1002590//Homo sapiens clone RG132J19, complete sequence.//1.1e-30:392:74//AC005163

R-HEMBB1002596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//8.5e-44:335:83//AL021707

R-HEMBB1002600//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-105:470:96//AC005865

R-HEM BB1002601//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//1.3e-44:445:77//AC004223

R-HEM BB1002603//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//7.0e-40:321:82//AC006162

R-HEM BB1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sapiens genomic clone 2347D7, genomic survey sequence.//1.1e-44:234:98//AQ060197

R-HEM BB1002610//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//7.0e-22:455:65//U91321

R-HEM BB1002613//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.0e-72:302:85//AC005908

R-HEM BB1002614//Homo sapiens 12q13.1 PAC RPCI11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.8e-10:512:60//AC004801

R-HEM BB1002617//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-24:486:63//AC005520

R-HEM BB1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.4e-41:326:83//AC004953

R-HEM BB1002635//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//2.6e-42:360:80//AC005910

R-HEM BB1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//9.1e-51:335:87//AF042090

R-HEM BB1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//0.0011:399:59//AF030694

R-HEM BB1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//4.1e-55:515:76//AF042090

R-HEM BB1002684//Human BAC clone RG066D11 from 7q22, complete sequence.//

1.7e-18:504:62//AC002430

R-HEMBB1002686//Homo sapiens full length insert cDNA clone ZC65D06.//7.0e-85:413:99//AF086217

R-HEMBB1002692//Homo sapiens 12p13.3 BAC RPCI11-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.8e-69:505:82//AC006206

R-HEMBB1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.26:390:58//AC004153

R-HEMBB1002699//Human NFE genomic fragment.//8.0e-32:226:79//M98511

R-HEMBB1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens genomic clone 344K23, genomic survey sequence.//8.6e-43:351:80//B59764

R-HEMBB1002705//Plasmodium yoelii rhoptry protein, complete cds.//0.0064:454:59//L27838

R-HEMBB1002712//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//9.6e-09:187:67//Z98052

R-MAMMA1000009//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.1e-21:201:80//AC005037

R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence.//4.2e-48:306:82//AF015720

R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//1.4e-41:306:86//AL022163

R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.//6.1e-36:281:83//AL031058

R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.3e-67:321:88//AC000090

R-MAMMA1000045//Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.//6.7e-86:559:86//AC004054

R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bcamicro1.//0.79:63:77//AF025889

R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 Syn GAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence.//1.6e-53:397:83//AL021366

R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.0e-37:295:83//AC005057

R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//7.1e-45:296:88//AC005867

R-MAMMA1000085

R-MAMMA1000092//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE.//8.2e-34:539:69//AL034410

R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//3.4e-39:297:85//AC003976

R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon 5.//2.6e-07:162:67//U69641

R-MAMMA1000129//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.1e-13:141:80//AC004882

R-MAMMA1000133

R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.7e-18:171:80//AC005328

R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-49:366:75//AC005000

R-MAMMA1000143//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC D9.2, WORKING DRAFT SEQUENCE.//3.9e-56:318:89//AJ009615

R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTS, STSS, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//2.1e-68:562:78//AL022476

R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.3e-06:408:58//AC005089

R-MAMMA1000171//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.5e-42:173:89//AQ037381

R-MAMMA1000173

R-MAMMA1000175//H.sapiens CpG island DNA genomic MseI fragment, clone 186c5, reverse read cpg186c5.rt1b.//0.072:90:72//Z57594

R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//1.5e-44:445:75//AC004552

R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence.//1.9e-23:135:85//AF038667

R-MAMMA1000221//HS_3242_B2_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, genomic survey sequence.//0.031:167:67//AQ220385

R-MAMMA1000227//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1071N3, WORKING DRAFT SEQUENCE.//4.5e-36:487:71//AL031728

R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq

21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideaemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//6.2e-07:445:59//AL022401

R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complete sequence.//1.6e-25:390:69//AC005266

R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//1.1e-37:327:80//AL008715

R-MAMMA1000257//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//1.3e-22:281:74//AL034549

R-MAMMA1000264//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.7e-29:337:67//AC003656

R-MAMMA1000266//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE.//7.7e-37:339:80//AL031670

R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.2e-40:283:86//AF001549

R-MAMMA1000277//CIT-HSP-516K6.TP CIT-HSP Homo sapiens genomic clone 516K6, genomic survey sequence.//3.0e-29:265:80//B49900

R-MAMMA1000278//Sequence 25 from patent US 5708157.//2.6e-39:282:82//I80056

R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000284//CITBI-E1-2522B20.TF CITBI-E1 Homo sapiens genomic clone

2522B20, genomic survey sequence.//1.8e-11:288:61//AQ280722
R-MAMMA1000287
R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete
sequence.//4.1e-16:169:77//AC005553
R-MAMMA1000307//RPCI11-89L1.TV RPCI11 Homo sapiens genomic clone R-89L1,
genomic survey sequence.//1.3e-86:429:97//AQ284795
R-MAMMA1000309//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spl
iced isoform of Jagged2, complete cds.//0.00020:384:60//AF029779
R-MAMMA1000312//Ichneutes sp. 16S ribosomal RNA gene, partial sequence./
/0.0026:310:60//AF003518
R-MAMMA1000313//Human cosmid Xq28_IA649, complete sequence.//1.5e-26:317
:67//U82694
R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUENCE, 5
unordered pieces.//3.1e-39:277:86//AC004947
R-MAMMA1000339//Homo sapiens clone HS19.1 Alu-Ya5 sequence.//3.2e-44:180
:89//AF015147
R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of 73 of
the complete sequence.//0.97:293:64//AE001388
R-MAMMA1000348//Homo sapiens BAC129, complete sequence.//4.4e-27:365:72/
/U85195
R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)),
complete sequence.//0.73:332:61//AC002493
R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete
sequence.//4.6e-80:279:89//AC005189
R-MAMMA1000361//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 753D4, WORKING DRAFT SEQUENCE.//7.8e-18:346:63//AL031676
R-MAMMA1000372//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone Y214H10, WORKING DRAFT SEQUENCE.//5.3e-40:299:83//AL022344
R-MAMMA1000385//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 310013, WORKING DRAFT SEQUENCE.//1.0e-28:225:84//AL031658
R-MAMMA1000388//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 232
1D3, genomic survey sequence.//4.7e-60:298:99//AQ038102
R-MAMMA1000395
R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete
sequence.//1.4e-84:276:88//AC004692
R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete
sequence.//6.7e-35:360:76//AC002394
R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842_A_23, complet
e sequence.//3.1e-69:327:79//AC004662
R-MAMMA1000414//Homo sapiens DNA sequence from PAC 164L12 on chromosome
Xq13.1-Xq21.2. Contains GSS (BAC end sequence),STS.//3.6e-41:180:87//AL0
09028
R-MAMMA1000416//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4
unordered pieces.//3.1e-59:478:77//AC005377
R-MAMMA1000421//Human coxVIb gene, last exon and flanking sequence.//5.3
e-53:294:82//X58139
R-MAMMA1000422//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 8B22, WORKING DRAFT SEQUENCE.//1.0:252:59//AL031737
R-MAMMA1000423//Homo sapiens clone DA0065G23, complete sequence.//2.0e-5
0:491:76//AC004816
R-MAMMA1000424//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-
27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STS
s and a polymorphic CA repeat.//3.5e-40:340:80//Z98950
R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//0.0019:87:79//AF0
62484
R-MAMMA1000431//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5
unordered pieces.//2.0e-58:564:77//AC004821
R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete sequenc

e.//3.0e-43:328:83//AC002067

R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequence.//0.9
5:209:65//U82672

R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone
: MXK3, complete sequence.//0.99:182:61//AB019236

R-MAMMA1000468

R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9N34, g
enomic survey sequence.//1.0e-38:142:88//AG010148

R-MAMMA1000478//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 169I5, WORKING DRAFT SEQUENCE.//1.3e-37:286:83//Z93015

R-MAMMA1000483//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384
B14, genomic survey sequence.//4.3e-34:158:86//B54637

R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete se
quence.//4.2e-98:569:90//AC006130

R-MAMMA1000500//Human BRCA1, Rho7 and vatl genes, complete cds, and ipf3
5 gene, partial cds.//1.2e-41:334:79//L78833

R-MAMMA1000501//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 153G14, WORKING DRAFT SEQUENCE.//1.4e-38:250:84//AL031118

R-MAMMA1000516//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 424J12, WORKING DRAFT SEQUENCE.//1.3e-43:318:83//Z82207

R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome 1p33-
34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.//4.4e-13:
202:73//AL031289

R-MAMMA1000559//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 169I5, WORKING DRAFT SEQUENCE.//2.2e-30:245:83//Z93015

R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01_183_B_7 map 10
q24, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.6e-39:281:80//U82205

R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, complete cds
.//9.2e-19:216:76//U18419

R-MAMMA1000576

R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//5.4e-53:297:85//AC005666

R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-35:450:71//AC006018

R-MAMMA1000594//Homo sapiens *** SEQUENCING IN PROGRESS *** from cosmid 5L5, WORKING DRAFT SEQUENCE.//4.3e-26:293:75//AJ009613

R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clone 2341F4, genomic survey sequence.//0.83:110:70//AQ057131

R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.6e-50:290:86//AC004956

R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic clone 2334J18, genomic survey sequence.//0.76:132:65//AQ038364

R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, partial sequence.//6.8e-06:431:59//U06970

R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U88573

R-MAMMA1000623

R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complete sequence.//3.3e-07:325:63//AC005498

R-MAMMA1000643//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39B17, WORKING DRAFT SEQUENCE.//1.4e-06:236:68//AL023656

R-MAMMA1000664//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0326F06; HTGS phase 1, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-40:338:81//AC004555

R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GS S, CpG island, complete sequence.//1.2e-46:327:86//AL021578

R-MAMMA1000670

R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome 6p24.
Contains STSs and GSSs, complete sequence.//2.2e-29:328:76//AL031785
R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:247:63
//AF054623
R-MAMMA1000696//Human Chromosome X clone bWXd173, WORKING DRAFT SEQUENCE
, 2 ordered pieces.//2.7e-46:464:71//AC004387
R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 u
nordered pieces.//3.4e-09:244:66//AC005075
R-MAMMA1000713//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5
unordered pieces.//3.7e-51:439:74//AC005478
R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, complete
sequence.//2.8e-29:288:75//AC004694
R-MAMMA1000718//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics
) , PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5
(from Lawrence Livermore), complete sequence.//3.0e-37:231:91//AC002366
R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequ
ence.//1.4e-35:299:81//AC005781
R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome Xp11.
2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protei
n pseudogene, EST, GSS, complete sequence.//3.9e-59:409:79//AL022163
R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 u
nordered pieces.//9.4e-29:560:66//AC005077
R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10
unordered pieces.//2.4e-14:309:68//AC004832
R-MAMMA1000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 732E4, WORKING DRAFT SEQUENCE.//4.1e-29:377:71//AL008722
R-MAMMA1000734//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 191J18, WORKING DRAFT SEQUENCE.//2.0e-108:420:99//AL024507
R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus.//6.6e-4

1:347:82//U03115

R-MAMMA1000744//T2708-T7 TAMU Arabidopsis thaliana genomic clone T2708, genomic survey sequence.//0.095:367:60//B20150

R-MAMMA1000746//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//7.4e-95:569:87//AC004661

R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.3e-48:295:84//AC003071

R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//5.7e-45:347:82//Z82178

R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.1e-32:292:80//U73169

R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.5e-50:467:79//AC005412

R-MAMMA1000776//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//1.0e-63:429:79//AC002454

R-MAMMA1000778//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.//3.5e-25:234:81//Z95704

R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//0.0021:119:74//AL031120

R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3.//6.3e-08:269:64//AJ229042

R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//1.1e-36:261:80//AC005339

R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic clone 2387J3, genomic survey sequence.//0.68:156:65//AQ240807

R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726_0_12, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.6e-50:335:86//AC005517

R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//1.3e-40:322:77//U91323

R-MAMMA1000842//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//4.1e-44:471:74//Z97985

R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.85:394:60//AC004815

R-MAMMA1000845//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.54:303:63//AL031744

R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete sequence.//1.7e-10:115:83//AF030876

R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//5.0e-44:352:83//AC004263

R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complete sequence.//1.8e-10:149:74//AC004611

R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16.//8.1e-05:205:66//AF009075

R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//2.9e-49:421:80//AC002364

R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//9.1e-41:302:83//AC002301

R-MAMMA1000867//Human BRCA1, Rho7 and vatl genes, complete cds, and ipf3 5 gene, partial cds.//1.9e-17:500:61//L78833

R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LANL), complete sequence.//1.2e-17:211:74//AC004653

R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//4.7e-09:160:65//AC003658

R-MAMMA1000877//Homo sapiens DNA sequence from PAC 958B3 on chromosome X p22.11-Xp22.22. Contains ESTs STS and CpG island.//3.2e-34:354:75//Z9302

3

R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.4e-41:411:74//AC002425

R-MAMMA1000883

R-MAMMA1000897

R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence.//1.3e-73:304:91//AC004506

R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F14150, genomic sequence, complete sequence.//8.4e-23:194:83//AC003110

R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ416i6, complete sequence.//1.5e-09:170:71//AC003024

R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//8.3e-13:323:67//AC005247

R-MAMMA1000921//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//6.8e-28:333:72//AL034379

R-MAMMA1000931//HS_3227_B1_B03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=D, genomic survey sequence.//1.4e-55:443:79//AQ191777

R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:340:84//AC005046

R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.8e-53:330:84//AC002347

R-MAMMA1000942//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:391:74//AC004383

R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.6e-75:566:81//AC002477

R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence.//0.013:285:59//AL034559

R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10

unordered pieces.//5.2e-45:288:90//AC005096

R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5
unordered pieces.//2.9e-108:561:96//AC006001

R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete sequenc
e.//3.9e-41:287:87//AC004263

R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chromosome
6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternati
vely spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MA
PK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islan
ds, complete sequence.//9.4e-65:542:79//Z95152

R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L1
5, BAC clone 7B7, complete sequence bases 1..333303.//3.2e-34:296:80//AJ
011930

R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequenc
e.//1.7e-40:255:87//AF088219

R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete seq
uence.//2.5e-39:315:73//AC005190

R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p
11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101

R-MAMMA1001008//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRA
FT SEQUENCE.//7.9e-88:432:98//AJ011929

R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete seq
uence.//3.8e-39:286:87//AC004910

R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6
unordered pieces.//2.0e-31:274:80//AC004913

R-MAMMA1001030//Homo sapiens full length insert cDNA clone ZD96C01.//3.2
e-99:469:99//AF088074

R-MAMMA1001035//RPCI-1-46G8Sp6 RPCI-1 Homo sapiens genomic clone RPCI-1-
46G8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285

R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089

R-nnnnnnnnnnnnn

R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394

R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125

R-MAMMA1001067//CIT-HSP-2371K20.TF CIT-HSP Homo sapiens genomic clone 2371K20, genomic survey sequence.//7.2e-65:346:95//AQ111326

R-MAMMA1001073

R-MAMMA1001074//Homo sapiens BAC clone NH0400010 from Y, complete sequence.//8.6e-33:457:69//AC006040

R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.15:325:62//AC004605

R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.6e-45:344:84//AC005609

R-MAMMA1001082//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403

R-MAMMA1001091//Sequence 7 from patent US 5468610.//0.0027:159:64//I15499

R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.//2.0e-51:267:82//AC005951

R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GT R2-2), 5' UTR. ESTs, STS.//6.9e-22:178:85//Z99570

R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPC1169K15, complete sequence.//3.0e-19:141:81//AC003963

R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2 gene, genomic sequence, complete sequence.//2.2e-46:462:75//AC003109

R-MAMMA1001133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE.//1.8e-68:455:86//AL031847

R-MAMMA1001139//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//7.1e-09:100:84//AL022345

R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7.//1.9e-49:362:85//U73684

R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.//9.5e-49:512:74//AC005922

R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-88D1 complete genomic sequence, complete sequence.//1.5e-29:305:76//AC002289

R-MAMMA1001161//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//1.1e-64:339:90//AL031286

R-MAMMA1001162//Human DNA from cosmid DNA MMDB (f10080) and MMDC (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis).//3.4e-09:243:64//M89651

R-MAMMA1001181//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.7e-29:351:74//AC004387

R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//AC006125

R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.99:243:61//AE000662

R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:223:86//U29156

R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748

R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING
DRAFT SEQUENCE, 2 ordered pieces.//8.9e-61:567:78//AC005412

R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), c
omplete sequence.//4.6e-08:442:61//AC004763

R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete
sequence.//1.3e-117:564:97//AC005393

R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library C
Homo sapiens genomic clone Plate=CT 802 Col=19 Row=M, genomic survey seq
uence.//6.0e-16:276:68//B33708

R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12,
genomic survey sequence.//0.041:277:61//B97762

R-MAMMA1001243

R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library C
Homo sapiens genomic clone Plate=CT 780 Col=2 Row=M, genomic survey sequ
ence.//3.5e-05:104:74//B43862

R-MAMMA1001249//H.sapiens DNA for matrix attachment region.//0.0013:95:7
5//Z54221

R-MAMMA1001256//Human BAC clone GS188P18, complete sequence.//3.4e-32:35
6:74//AC000115

R-MAMMA1001259

R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//6
.3e-20:226:75//AB014561

R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Co
ntains ESTS, CA repeat.//1.1e-47:352:85//Z95124

R-MAMMA1001271

R-MAMMA1001274//H.sapiens DNA for trapped exon (ID HMC07C06), genomic su
rvey sequence.//3.1e-40:232:93//X88457

R-MAMMA1001280//Homo sapiens full length insert cDNA clone YW26C09.//1.9
e-112:574:95//AF087976

R-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//2.9e-114:582:96//AL022314

R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, STSSs, a BAC end-sequence (GSS) and a CA repeat polymorphism.//1.9e-64:268:88//AL008730

R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.5e-38:306:83//AC005703

R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat.//1.5e-37:306:82//Z83838

R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//2.4e-15:260:71//AL022398

R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83//AC005614

R-MAMMA1001330//Human BAC clone RG066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430

R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 20q12-13.2. Contains Krs-2, K+ channel protein, stress responsive.//1.3e-24:137:81//Z93016

R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete

sequence.//5.4e-51:197:89//AC002041
R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//0.99:182:64//AC004685
R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42:303:86//AC004815
R-MAMMA1001388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//1.5e-44:324:83//AL021707
R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SEQUENCE.//2.0e-39:254:89//AP000044
R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.4e-36:251:88//AC005805
R-MAMMA1001411//T15F1-T7.1 TAMU Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.//1.0:98:71//AQ248928
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96//AF038957
R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//2.8e-09:377:63//AC005179
R-MAMMA1001435//S.pombe chromosome I cosmid c26H5.//1.0:356:59//Z99126
R-MAMMA1001442//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//3.4e-17:259:72//AC004047
R-MAMMA1001446//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.9e-17:231:71//AC004491
R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:73//AL024493
R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-2F3, genomic survey sequence.//3.0e-23:141:96//B04295
R-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//3.4e-09:

309:64//L31783

R-MAMMA1001487//Homo sapiens chromosome 17, clone hRPC.1108_L_11, complete sequence.//5.1e-30:286:79//AC005206

R-MAMMA1001501

R-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B7, WORKING DRAFT SEQUENCE.//4.3e-19:349:64//AL031714

R-MAMMA1001510

R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBNL H194), complete sequence.//1.5e-09:136:75//AC005352

R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:300:84//AC002418

R-MAMMA1001551//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-57:282:89//AL020997

R-MAMMA1001575

R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.6e-60:530:78//M61764

R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds.//1.3e-29:161:86//U78027

R-MAMMA1001600//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.1e-18:390:66//AC004216

R-MAMMA1001604//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSSs, GSSs and a putative CpG island, complete sequence.//1.0:227:62//AL022238

R-MAMMA1001606//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.3e-17:219:69//AL031985

R-MAMMA1001620//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//2.1e-51:298:84//AL031650

R-MAMMA1001627//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//7.8e-45:328:85//Z86090

R-MAMMA1001630//, complete sequence.//2.5e-08:170:72//AC005399

R-MAMMA1001633//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10 q25, complete sequence.//2.2e-21:241:70//AC005386

R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromosome X p11.3. Contains EST, STS and GSS, complete sequence.//1.1e-32:346:74//Z84466

R-MAMMA1001649

R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence.//9.4e-68:267:89//AC004811

R-MAMMA1001670//Human DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSS and CpG islands.//1.7e-49:322:88//Z82216

R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//2.4e-114:575:96//AC005614

R-MAMMA1001679//CIT-HSP-2335N4.TF CIT-HSP Homo sapiens genomic clone 2335N4, genomic survey sequence.//2.4e-82:400:99//AQ037393

R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.7e-47:533:72//AC004166

R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.6e-12:194:72//AC005261

R-MAMMA1001692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//9.6e-44:414:77//AL022345

R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, complete sequence.//3.1e-31:436:70//AF110324

R-MAMMA1001715//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 73E16, WORKING DRAFT SEQUENCE.//8.8e-76:524:84//Z95330
R-MAMMA1001730
R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta tubul
in (clone B9T), partial.//2.7e-13:382:63//X60786
R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21
/28, WORKING DRAFT SEQUENCE.//3.9e-47:318:87//AP000050
R-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence.//4.0e-1
08:566:95//AC006017
R-MAMMA1001744
R-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequen
ce.//3.5e-113:564:97//AF070718
R-MAMMA1001751//Homo sapiens chromosome 19, cosmid R27328, complete sequ
ence.//3.6e-30:312:75//AC005625
R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform
(SFD) mRNA, complete cds.//4.7e-34:320:77//AF041338
R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4_G_17, complete
sequence.//4.7e-10:244:67//AC003688
R-MAMMA1001760//RPCI11-38L16.TV RPCI-11 Homo sapiens genomic clone RPCI-
11-38L16, genomic survey sequence.//1.3e-10:236:64//AQ029432
R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 geno
mic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.74:361:60/
/AC005140
R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPK.147_L_13, complet
e sequence.//1.6e-42:416:76//AC005332
R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073_F_15, comple
te sequence.//1.4e-13:129:83//AC004686
R-MAMMA1001771//M.musculus mRNA for semaphorin B.//1.1e-34:530:69//X8599
1
R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT

SEQUENCE, 17 unordered pieces.//1.1e-42:282:85//AC000360

R-MAMMA1001785//Human chromosome 16p13.11 BAC clone CIT987SK-98H8 complete sequence.//3.0e-49:282:86//U91319

R-MAMMA1001788

R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//9.8e-43:530:71//AC004913

R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.8e-43:324:79//AC004020

R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of 73 of the complete sequence.//0.65:183:63//AE001432

R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:417:62//AC005018

R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.6e-40:313:84//AC005859

R-MAMMA1001818

R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.2e-45:340:82//AC004086

R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-53:291:85//AC004966

R-MAMMA1001836//HS_3164_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=B, genomic survey sequence.//6.5e-08:79:89//AQ185484

R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//8.4e-55:309:85//AC003682

R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, complete sequence.//1.6e-16:125:90//AC006144

R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:516:74//AC002099

R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.7e-38:308:82//AC002425

R-MAMMA1001858//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//6.5e-50:283:86//U80460

R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone pDJ398g19, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.4e-36:224:86//AC005143

R-nnnnnnnnnnnnn//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//1.4e-11:495:63//AE001417

R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.2e-42:446:76//AC003117

R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKN A1, CDKN1, MDA-6, SDI1, PIC1, CAP20) genes. Contains probable GTPase and receptor genes and ESTs, STSS and CpG islands.//6.9e-44:391:78//Z85996

R-MAMMA1001880//Human DNA sequence from fosmid F77D12 on chromosome 22q12-qter contains ESTs, tRNA.//1.3e-15:181:76//Z82097

R-MAMMA1001890//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-670B5 complete genomic sequence, complete sequence.//1.7e-43:283:86//AC002303

R-MAMMA1001907//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 385E7, WORKING DRAFT SEQUENCE.//1.4e-48:420:79//AL031720

R-nnnnnnnnnnnnn//Saccharomyces cerevisiae chromosome IV cosmid 9481.//2.9e-14:505:60//U28373

R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:63//AF041008

R-MAMMA1001956//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//1.4e-51:422:79//AL034380

R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163:91//AF015149

R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequ

ence, complete sequence.//8.7e-10:186:76//AC002128
R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:86//AC003071
R-MAMMA1001992//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-44:525:72//AC004581
R-MAMMA1002009//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109G6, WORKING DRAFT SEQUENCE.//1.4e-43:282:79//AL023879
R-MAMMA1002011
R-MAMMA1002032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//1.1e-39:310:84//AL031284
R-MAMMA1002033//Homo sapiens chromosome 5, Pac clone 162o17 (LBNL H147), complete sequence.//2.5e-17:170:81//AC003954
R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence.//8.7e-79:296:85//AC004865
R-MAMMA1002042//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//8.8e-46:386:80//U91318
R-MAMMA1002047//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//1.9e-32:326:75//U91318
R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506_H_21, complete sequence.//6.6e-48:367:82//AC005962
R-MAMMA1002058//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.25:139:69//AC005052
R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-45:406:78//AC004676
R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//2.3e-22:357:64//AC005291
R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//2.5e-38:304:82//AC004263
R-MAMMA1002084//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 1174N9, WORKING DRAFT SEQUENCE.//8.9e-41:319:83//AL031602
R-MAMMA1002093//CIT-HSP-2060J9.TF CIT-HSP Homo sapiens genomic clone 206
0J9, genomic survey sequence.//9.7e-17:129:88//B69983
R-MAMMA1002108
R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22
Contains ESTs, complete sequence.//0.94:168:64//Z73495
R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete
sequence.//4.8e-40:313:83//AC005670
R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, comple
te sequence.//2.0e-70:461:83//AC004953
R-MAMMA1002140//Human DNA sequence from PAC 465G10 on chromosome X conta
ins Menkes Disease (ATP7A) putative Cu++-transporting P-type ATPase exon
s 2 to 21, PGAM-B, ESTs.//1.1e-32:477:73//Z94801
R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase
gene, promoter region and exon 1.//6.6e-06:130:73//AF027357
R-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 126A5, WORKING DRAFT SEQUENCE.//6.0e-19:242:73//AL031447
R-MAMMA1002153//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4
, BAC clone C0281M17; HTGS phase 1, WORKING DRAFT SEQUENCE, 3 unordered
pieces.//2.1e-51:291:75//AC006052
R-MAMMA1002155//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 608E8, WORKING DRAFT SEQUENCE.//1.2e-53:461:79//AL022343
R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, compl
ete sequence.//5.1e-37:305:82//AC004997
R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 20q1
2-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear recep
tor coactivator gene, ESTs, STSs, GSSs, complete sequence.//8.1e-34:296:
81//AL034418
R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13

.2-13.33. Contains the 3' part of a gene for the ortholog of mouse trans membrane receptor Celsrl, a novel gene for a protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases, and the 3' part of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.9e-39:332:82//AL031588

R-MAMMA1002174//Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.//4.4e-12:189:72//AC005871

R-MAMMA1002198//Homo sapiens clone DJ0800G07, complete sequence.//1.1e-48:338:81//AC004890

R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//1.2e-23:269:74//AC005821

R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:243:68//AC005158

R-MAMMA1002219//Homo sapiens 12p13.3 RPCI4-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.3e-45:295:88//AC004802

R-MAMMA1002230//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//7.3e-41:385:78//AL034379

R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//7.3e-45:363:79//U38253

R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//2.8e-119:582:98//AC005666

R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//4.7e-42:319:84//AC005600

R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.5e-33:571:67//AC006120

R-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//2.3e-35:462:70//AF068749

R-MAMMA1002269//345I17.TV CIT978SKA1 Homo sapiens genomic clone A-345I17

, genomic survey sequence.//4.7e-05:153:69//B15590

R-MAMMA1002282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE.//8.5e-37:467:71//Z85987

R-MAMMA1002292//Hordeum vulgare lipoxxygenase 2 (LoxC) mRNA, complete cds .//0.074:178:61//L37358

R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:355:71//AC005568

R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.2e-35:281:82//AC004231

R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//6.7e-48:381:80//Z69375

R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from 7q11.23, complete sequence.//1.8e-17:296:70//AC005074

R-MAMMA1002299//HS_3116_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=14 Row=K, genomic survey sequence.//4.1e-60:354:91//AQ140526

R-MAMMA1002308

R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat and STS, complete sequence.//9.9e-35:283:83//Z73979

R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.3e-86:503:90//AC006210

R-MAMMA1002312//H.sapiens gene encoding La autoantigen.//1.3e-23:382:67//X97869

R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSS and GSSs, complete sequence.//1.3e-59:323:87//AL031054

R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756

R-MAMMA1002322//Homo sapiens genomic DNA, chromosome 21q11.1, segment 13 /28, WORKING DRAFT SEQUENCE.//2.3e-48:452:76//AP000042

R-MAMMA1002329//M.musculus mRNA for semaphorin B.//2.0e-12:210:73//X8599
1

R-MAMMA1002332//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//3.4e-46:393:71//AC004973

R-MAMMA1002333//HS_3245_A1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=7 Row=C, genomic survey sequence.//3.1e-21:146:92//AQ205759

R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//9.7e-39:310:79//AF001549

R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPCI3-305I20 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-46:443:76//AC006088

R-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//1.1e-90:553:89//AL022100

R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2.//8.8e-81:388:92//Y15228

R-MAMMA1002353//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//5.5e-35:302:80//AC002996

R-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//5.4e-52:361:76//Z93241

R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//8.3e-28:187:91//AC004662

R-MAMMA1002359//Human DNA sequence from cosmid L118D5, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//Z68869

R-MAMMA1002360//HS_2163_B2_C08_MR CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=2163 Col=16 Row=F, genomic survey sequence.//1.5e-20:374:66//AQ125213

R-MAMMA1002361//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//2.2e-35:264:85//AL033520

R-MAMMA1002362//H.sapiens PEX gene.//1.8e-40:243:86//Y10196

R-MAMMA1002380//RPCI11-73J4.TJ RPCI11 Homo sapiens genomic clone R-73J4, genomic survey sequence.//1.7e-38:295:77//AQ268168

R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-37:311:81//AC004801

R-MAMMA1002385

R-MAMMA1002392//Human BAC clone RG066D11 from 7q22, complete sequence.//2.0e-37:365:77//AC002430

R-MAMMA1002411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//9.4e-22:496:65//AL031668

R-MAMMA1002413//Homo sapiens 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.3e-15:153:77//AC005146

R-MAMMA1002417//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.8e-23:508:62//AL020997

R-MAMMA1002427//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.5e-37:288:84//U91321

R-MAMMA1002428//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//6.0e-05:130:75//AL034423

R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains HB15 gene, ESTs, CA repeat, STS and GSS.//4.8e-18:205:78//AL022396

R-MAMMA1002446//CIT-HSP-2021L14.TR CIT-HSP Homo sapiens genomic clone 20

21L14, genomic survey sequence.//4.6e-41:387:72//B65379
R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence.//1.2e-67:491:82//AC005512
R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//1.4e-28:188:85//AC003982
R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//6.3e-09:280:61//U10556
R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//1.5e-25:310:74//Z83822
R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-98:533:93//AC005077
R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.7e-114:560:97//AF055460
R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//2.1e-46:329:84//Z69375
R-MAMMA1002498//Rat mRNA.//0.0068:223:64//M59859
R-MAMMA1002524//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:460:60//AC005139
R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.2e-101:529:95//AF065214
R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds.//6.6e-50:471:77//AF041427
R-MAMMA1002554//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//5.7e-38:279:84//AC004056
R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete sequence.//9.6e-13:237:67//AC005878
R-MAMMA1002566//CITBI-E1-2509P21.TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey sequence.//9.7e-14:216:73//AQ261427

R-MAMMA1002571//CITBI-E1-2516L21.TF CITBI-E1 Homo sapiens genomic clone
2516L21, genomic survey sequence.//4.6e-25:142:99//AQ279542

R-MAMMA1002573//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 811H13, WORKING DRAFT SEQUENCE.//1.1e-30:250:82//AL023805

R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end.
//1.0:196:61//M58580

R-MAMMA1002590//H.sapiens CpG island DNA genomic MseI fragment, clone 8d
5, forward read cpg8d5.flg.//1.0:114:64//Z63758

R-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1103G7, WORKING DRAFT SEQUENCE.//9.0e-96:459:98//AL034548

R-MAMMA1002598//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 120G22, WORKING DRAFT SEQUENCE.//0.79:362:58//AL031847

R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete
sequence.//1.3e-46:333:80//AC005803

R-MAMMA1002612//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 269M15, WORKING DRAFT SEQUENCE.//7.4e-41:283:86//AL021395

R-MAMMA1002617//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 591N18, WORKING DRAFT SEQUENCE.//1.7e-20:308:71//AL031594

R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence.//1.2e-31
:230:76//AC005067

R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.0e-1
13:551:98//AJ010598

R-MAMMA1002622//Homo sapiens chromosome 4 clone B207D4 map 4q25, complet
e sequence.//2.8e-43:324:83//AC004050

R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171_I_10, comple
te sequence.//2.7e-80:344:84//AC004687

R-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1056L3, WORKING DRAFT SEQUENCE.//2.6e-34:391:72//AL031727

R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmid

s R32543, , and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//5.5e-58:346:81//AC003006

R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-52:285:92//AC004895

R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//2.1e-13:359:64//AF055666

R-MAMMA1002646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 394I7, WORKING DRAFT SEQUENCE.//2.5e-24:285:68//AL023585

R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11.//0.64:237:61//X03424

R-MAMMA1002655//Homo sapiens minisatellite ceb1 repeat region.//0.18:152:65//AF048727

R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence.//2.5e-46:370:82//AC004870

R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//7.4e-55:298:92//Z92844

R-MAMMA1002671//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411

R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome X q25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//3.1e-38:410:76//AL022162

R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.4e-107:544:96//D86987

R-MAMMA1002685//HS_2052_A1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=3 Row=0, genomic survey sequence.//1.2e-23:255:75//AQ231087

R-MAMMA1002698//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.1e-38:299:83//AC004673

R-MAMMA1002699//Mus musculus intersectin-EH binding protein Ibp1 mRNA, partial cds.//3.3e-05:61:93//AF057285

R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//3.5e-39:317:81//AB011399

R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPCI5-977L1 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.26:365:62//AC005293

R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13.//2.5e-31:304:77//AJ006995

R-MAMMA1002721//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//2.3e-40:279:87//Z83826

R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.45:183:64//AC004710

R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.1e-42:410:74//AC002037

R-MAMMA1002744//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.6e-19:473:63//U96629

R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//2.2e-108:544:97//AC005856

R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-106:551:95//AC006055

R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-34:305:79//AC005020

R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.00014:130:74//U95626

R-MAMMA1002764//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//8.7e-10:118:81//AC005781

R-MAMMA1002765//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//1.2e-31:290:78//AC006128

R-MAMMA1002769//Human DNA sequence from PAC 36J3, between markers DXS119 2 and DXS102 on chromosome X.//0.94:260:62//Z82975

R-MAMMA1002780//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//2.6e-21:529:62//AL031667

R-MAMMA1002782//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE.//2.8e-30:234:72//AL022320

R-MAMMA1002796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 237J2, WORKING DRAFT SEQUENCE.//1.0:155:66//AL021394

R-MAMMA1002807//Human DNA sequence from BAC 941F9 on chromosome 22q11.2-pter. Contains ESTs, STSs and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island, complete sequence.//5.0e-42:443:75//Z95331

R-MAMMA1002820//345M16.TVB CIT978SKA1 Homo sapiens genomic clone A-345M16, genomic survey sequence.//1.3e-14:95:87//B17487

R-MAMMA1002830//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//4.1e-20:223:74//AC002073

R-MAMMA1002833//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.8e-37:295:84//AC005295

R-MAMMA1002835

R-MAMMA1002838//Human gene hY3 encoding a cytoplasmic Ro RNA.//4.4e-14:108:92//V00585

R-MAMMA1002842//CIT-HSP-2017022.TRB CIT-HSP Homo sapiens genomic clone 2017022, genomic survey sequence.//5.2e-43:168:85//B67141

R-MAMMA1002843//Homo sapiens clone GS051M12, complete sequence.//8.7e-44:525:71//AC005007

R-MAMMA1002844

R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end.//2.8e-99:361:91//X79067
R-MAMMA1002868//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2
unordered pieces.//9.6e-39:288:81//AC004906
R-MAMMA1002871//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, comple
te sequence.//0.0022:490:57//AC006044
R-MAMMA1002880//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Sys
tems Human BAC Library) complete sequence.//1.3e-09:143:76//AC005296
R-MAMMA1002881//Human thymopoietin (TMPO) gene, partial exon 6, complete
exon 7, partial exon 8, and partial cds for thymopoietin beta.//5.1e-41
:264:87//U18271
R-MAMMA1002886//Homo sapiens DNA sequence from PAC 168L15 on chromosome
6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS.
CpG island, complete sequence.//4.7e-32:216:90//AL022069
R-MAMMA1002887
R-MAMMA1002890
3.4e-49:376:81//AG006257
R-MAMMA1002892//Homo sapiens PAC clone DJ0765G07 from 7q11, complete seq
uence.//6.0e-60:344:79//AC004881
R-MAMMA1002895//RPCI11-90K13.TV RPCI11 Homo sapiens genomic clone R-90K1
3, genomic survey sequence.//2.1e-34:300:77//AQ283502
R-MAMMA1002908//Human Chromosome X, complete sequence.//4.2e-39:297:85//
AC004070
R-MAMMA1002909//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4
, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered
pieces.//3.4e-23:344:74//AC005798
R-MAMMA1002930//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete
sequence.//5.2e-39:261:88//AC006019
R-MAMMA1002938//C.pasteurianum gap gene.//1.0:343:59//X72219
R-MAMMA1002941//Homo sapiens chromosome 17, clone hRPK.346_K_10, complet

e sequence.//6.3e-88:556:87//AC006120

R-MAMMA1002947

0.48:156:69//AC005469

R-MAMMA1002964//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatas e-1, ESTs, and a CA repeat.//1.2e-39:473:73//AL020997

R-MAMMA1002970//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//4.7e-47:420:77//AC005200

R-MAMMA1002972//alpha 1 syntrophin [human, mRNA Partial, 1771 nt]../0.97:305:62//S81737

R-MAMMA1002973//Human DNA sequence from cosmid V210E9, between markers D XS366 and DXS87 on chromosome X.//2.6e-35:256:85//Z70280

R-MAMMA1002982

1.0e-27:110:85//AG005524

R-MAMMA1002987//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.4e-28:527:66//AC004460

R-MAMMA1003003//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.9e-48:418:78//AC006109

R-MAMMA1003004//, complete sequence.//2.0e-12:442:61//AC005406

R-MAMMA1003007//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.7e-48:293:91//AC006109

R-MAMMA1003011//A-306G8.TP CIT978SK Homo sapiens genomic clone A-306G8, genomic survey sequence.//0.45:168:64//B18092

R-MAMMA1003015//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.9e-44:399:77//AC005740

R-MAMMA1003019//RPCI11-9J9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-9J9, genomic survey sequence.//2.7e-14:294:68//B71583

R-MAMMA1003026//HS_2166_B2_C12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=24 Row=F, genomic survey sequence.//0.021:189:64//AQ125639

R-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//1.8e-98:525:95//AC005214

R-MAMMA1003035//Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore L L12NC01 or LL12NC02 human cosmid libraries) complete sequence.//6.7e-06:297:63//AC004550

R-MAMMA1003039//RPCI11-56J17.TJ RPCI11 Homo sapiens genomic clone R-56J17, genomic survey sequence.//0.21:375:59//AQ081889

R-MAMMA1003040//Human DNA sequence from cosmid L108f12, Huntington's Disease Region, chromosome 4p16.3.//2.7e-29:298:67//Z49235

R-MAMMA1003044//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//2.9e-14:113:91//AC004560

R-MAMMA1003047

R-MAMMA1003049

R-MAMMA1003055//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 377F16, WORKING DRAFT SEQUENCE.//2.3e-45:317:86//Z93783

R-MAMMA1003056//Homo sapiens chromosome 19, cosmid R34275, complete sequence.//1.0:229:63//AC005305

R-MAMMA1003057//M.domesticus MD6 mRNA.//6.2e-42:326:82//X54352

R-MAMMA1003066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//3.1e-49:299:87//Z83826

R-MAMMA1003089//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//2.7e-30:520:67//AC005084

R-MAMMA1003099//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey sequence.//4.2e-44:338:82//B71494

R-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//3.4e-48:423:79//U72634

R-MAMMA1003113//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//4.8e-114:567:97//AC006087

R-MAMMA1003127//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//1.4e-34:283:83//Z99716

R-MAMMA1003135//P.knowlesi Mbn-cutting sites in lambda KBS50.//0.010:243:62//M38776

R-MAMMA1003140//Homo sapiens chromosome 17, clone HCIT87G17, complete sequence.//6.7e-34:288:81//AC003663

R-MAMMA1003146//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//4.8e-08:438:59//M97514

R-nnnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE.//1.7e-63:149:94//AL021579

R-MAMMA1003166//HS_3128_A1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=1 Row=C, genomic survey sequence.//3.0e-17:261:70//AQ140766

R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence.//2.6e-111:593:94//AF070640

R-NT2RM4000024

R-NT2RM4000027//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//0.026:476:56//AC004993

R-NT2RM4000030//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.00044:378:59//U70653

R-NT2RM4000046//M.mulatta MHC DR beta 6 gene encoding major histocompatibility complex.//0.27:130:64//Z26239

R-NT2RM4000061

R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds.//7.2e-112:550:97//AF070639

R-NT2RM4000086//RPCI11-6J23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6J23, genomic survey sequence.//7.2e-18:277:71//B49463

R-NT2RM4000104//F.rubripes GSS sequence, clone 063K10aG5, genomic survey
sequence.//3.6e-08:287:61//Z88817

R-NT2RM4000139//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL),
complete sequence.//9.4e-08:336:65//AC005199

R-NT2RM4000155

R-NT2RM4000156//Homo sapiens chromosome 17, clone hRPK.136_H_19, complet
e sequence.//3.4e-23:335:72//AC005856

R-nnnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4
, complete cds.//1.6e-87:551:87//D12646

R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence.//5.9e-14:122
:88//L22154

R-NT2RM4000191

R-NT2RM4000197//HS_3241_A2_H05_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3241 Col=10 Row=0, genomic survey
sequence.//2.8e-86:430:97//AQ206812

R-NT2RM4000199//Mus musculus Yp BAC GSMB-368G7 (Genome Systems Mouse BAC
Library) complete sequence.//0.0047:193:63//AC006056

R-NT2RM4000200

R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), c
omplete sequence.//2.1e-40:334:76//AC004035

R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//5
.2e-102:546:94//AB018255

R-NT2RM4000215

R-nnnnnnnnnnnnn//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q
25.1, complete sequence.//2.1e-55:303:86//AC005383

R-NT2RM4000233//Struthio camelus microsatellite sequence OSM 7.//1.2e-07
:198:67//AF003735

R-NT2RM4000244//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323),
complete sequence.//1.7e-49:322:88//AC006116

R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 72f8 In DGCR R
egion, complete sequence.//0.97:184:66//AC000085

R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence.//
6.2e-66:552:78//AC000055

R-NT2RM4000290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 394I7, WORKING DRAFT SEQUENCE.//1.4e-05:229:65//AL023585

R-NT2RM4000324

R-NT2RM4000327//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 75N14, WORKING DRAFT SEQUENCE.//3.3e-42:443:75//Z97199

R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12
unordered pieces.//6.4e-64:433:84//AC004826

R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds.//7.7e-11:210
:69//D13630

R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8.//0.084:257:60//U500
66

R-NT2RM4000356

R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//8.
7e-112:577:95//AB014542

R-NT2RM4000368

1.6e-48:348:85//AG006257

R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds.//
4.4e-35:141:87//D42148

R-NT2RM4000395//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11
-8N9, genomic survey sequence.//1.4e-25:207:75//B71494

R-NT2RM4000414//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 228H13, WORKING DRAFT SEQUENCE.//7.1e-17:492:64//AL031985

R-NT2RM4000421//RPCI11-66B1.TK RPCI11 Homo sapiens genomic clone R-66B1,
genomic survey sequence.//1.8e-40:311:82//AQ241167

R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, W

ORKING DRAFT SEQUENCE, 35 unordered pieces.//2.5e-47:316:87//AC005867
R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.6e-17:133:78//AF062476
R-NT2RM4000457
R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//4.6e-113:559:96//AJ010952
R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22C.//0.00015:170:67//AB000461
R-NT2RM4000496
R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds.//0.21:290:58//M80829
R-NT2RM4000514//CIT-HSP-2169K4.TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey sequence.//1.5e-20:150:89//B95717
R-nnnnnnnnnnnn//HS-1024-B2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=2 Row=N, genomic survey sequence.//6.3e-10:74:98//B34556
R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12.//0.15:406:61//AF078790
R-NT2RM4000531
R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//1.0:119:66//AE001391
R-NT2RM4000534//paramecium species 4.51er mt dna dimer: replication initiation region, clone 2.//9.8e-05:326:60//K00909
R-NT2RM4000585//HS_3252_A2_G08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=16 Row=M, genomic survey sequence.//1.9e-69:376:93//AQ219890
R-NT2RM4000590//CIT-HSP-539024.TV CIT-HSP Homo sapiens genomic clone 539024, genomic survey sequence.//1.7e-38:226:93//B50657
R-NT2RM4000595//Human Chromosome X clone bWXd342, complete sequence.//1.

0:239:61//AC004072

R-NT2RM4000603//RPCI11-49P13.TK RPCI11 Homo sapiens genomic clone R-49P13, genomic survey sequence.//0.77:139:64//AQ051950

R-nnnnnnnnnnnnnnn

R-NT2RM4000616//HS_3107_A2_B03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=6 Row=C, genomic survey sequence.//1.3e-54:272:99//AQ210034

R-NT2RM4000674

R-NT2RM4000689//Mus musculus pericentrin mRNA, complete cds.//3.5e-70:551:80//U05823

R-NT2RM4000698

R-nnnnnnnnnnnnnnn

R-NT2RM4000712//Homo sapiens clone NH0512E16, complete sequence.//0.54:294:58//AC005039

R-NT2RM4000717//Plasmodium falciparum MAL3P8, complete sequence.//0.050:387:58//AL034560

R-NT2RM4000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.0e-107:566:95//AL034379

R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//1.1e-103:536:95//AB018303

R-NT2RM4000741//CIT-HSP-2294N4.TR CIT-HSP Homo sapiens genomic clone 2294N4, genomic survey sequence.//5.2e-41:244:93//AQ006361

R-NT2RM4000751//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//2.7e-28:416:67//AL034405

R-NT2RM4000764//Human HepG2 3' region MboI cDNA, clone hmd3g01m3.//2.1e-33:199:96//D17217

R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//0.00060:241:62//AC002980

R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//2

.9e-104:546:94//AB007920

R-NT2RM4000787//Homo sapiens, clone hRPK.3_A_1, complete sequence.//5.3e-32:321:77//AC006198

R-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//1.9e-111:552:97//AC005306

R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosmid Clone cos39, complete sequence.//0.74:364:57//U58675

R-NT2RM4000796//Homo sapiens full length insert cDNA clone ZD62D10.//2.7e-105:510:98//AF086348

R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end.//7.7e-27:158:96//M21868

R-NT2RM4000813

R-NT2RM4000820//, complete sequence.//2.0e-104:432:97//AC005406

R-NT2RM4000833//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MXI22, complete sequence.//2.0e-07:166:68//AB012248

R-NT2RM4000848//Rabies virus matrix (M) protein mRNA, complete cds.//0.073:70:84//M22013

R-NT2RM4000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:237:62//AC004709

R-NT2RM4000855

R-nnnnnnnnnnnnn//HS_3189_B2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=16 Row=D, genomic survey sequence.//2.1e-06:114:73//AQ300597

R-NT2RM4000895//Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.//3.8e-46:207:91//AF077058

R-NT2RM4000950//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.0:336:60//AC002530

R-NT2RM4000971//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A

5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing idurona
te 2-sulfatase gene and pseudogene, complete sequence.//7.1e-09:259:64//
AF011889

R-NT2RM4000979

R-NT2RM4000996//HS_3164_A1_E02_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3164 Col=3 Row=I, genomic survey s
equence.//2.0e-82:443:94//AQ141622

R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.
2e-112:545:97//AB018272

R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//7.
9e-113:556:97//AB014539

R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 genes.//1.2e-10:120:82//A
J224639

R-NT2RM4001047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 163G9, WORKING DRAFT SEQUENCE.//1.0:158:67//AL008733

R-NT2RM4001054//CIT-HSP-2292N8.TR CIT-HSP Homo sapiens genomic clone 229
2N8, genomic survey sequence.//5.8e-19:118:97//AQ004096

R-nnnnnnnnnnnnn//Mouse DNA with homology to EBV IR3 repeat, segment 1, cl
one Mu2.//1.0e-05:271:64//M10296

R-NT2RM4001092//CITBI-E1-2524J20.TR CITBI-E1 Homo sapiens genomic clone
2524J20, genomic survey sequence.//1.0:186:63//AQ277294

R-NT2RM4001116

R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete
sequence.//3.6e-79:468:90//AC004593

R-NT2RM4001151//HS_2270_B1_E05_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2270 Col=9 Row=J, genomic survey s
equence.//5.5e-62:312:98//AQ163739

R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKI
NG DRAFT SEQUENCE, 31 unordered pieces.//1.4e-107:536:97//AC005841

R-NT2RM4001160//HS_3015_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=19 Row=P, genomic survey sequence.//7.1e-35:201:95//AQ118712

R-NT2RM4001187//X.laevis xUBFbeta2 mRNA for upstream binding factor 1.//0.019:177:63//X57201

R-NT2RM4001191//HS_3002_A1_F05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey sequence.//3.9e-33:230:75//AQ088791

R-NT2RM4001200//Homo sapiens full length insert cDNA clone YL35H03.//7.5e-69:335:99//AF085857

R-NT2RM4001203

R-NT2RM4001204

R-NT2RM4001217

R-NT2RM4001256

R-NT2RM4001258

R-NT2RM4001309

R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPC11-71H24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.00055:183:63//AC004551

R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117_K_16, complete sequence.//4.5e-21:212:79//AC004757

R-NT2RM4001320//CIT-HSP-2303E22.TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey sequence.//3.8e-30:86:89//AQ021084

R-NT2RM4001340

0.0027:493:60//AC005133

R-NT2RM4001344

R-NT2RM4001347//CITBI-E1-2506I20.TR CITBI-E1 Homo sapiens genomic clone 2506I20, genomic survey sequence.//6.5e-16:101:99//AQ262797

R-NT2RM4001371//CITBI-E1-2503G21.TR CITBI-E1 Homo sapiens genomic clone

2503G21, genomic survey sequence.//0.063:140:65//AQ265776
R-NT2RM4001382//HS_3044_A1_F02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=3 Row=K, genomic survey sequence.//0.96:103:66//AQ098668
R-NT2RM4001384//R.norvegicus mRNA for dendrin.//8.5e-07:120:75//Y09000
R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment.//2.3e-15:199:75//M25920
R-NT2RM4001411//Rattus norvegicus FceRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds.//1.7e-55:235:83//U57391
R-NT2RM4001412
R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library) complete sequence.//1.7e-80:489:89//U69730
R-NT2RM4001437//RPCI11-56D2.TJ RPCI11 Homo sapiens genomic clone R-56D2, genomic survey sequence.//3.8e-43:250:93//AQ081969
R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//0.0034:224:63//AC005926
R-NT2RM4001454//Homo Sapiens Chromosome X clone bWXd90, complete sequence.//2.4e-33:360:68//AC004075
R-NT2RM4001455//HS_3229_B1_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=7 Row=J, genomic survey sequence.//1.0:183:61//AQ191289
R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.2e-51:451:79//AC005282
R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.2e-102:547:93//AB014585
R-NT2RM4001519//HS_2208_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=13 Row=K, genomic survey sequence.//0.25:214:63//AQ091836
R-NT2RM4001522//H.sapiens gene for Cu/Zn-superoxide dismutase.//3.6e-13:

246:70//Z29336

R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence.//0.055:320:58//AL008970

R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//3.9e-26:329:72//AC005910

R-NT2RM4001566//Human trophinin mRNA, complete cds.//6.3e-38:296:86//U04811

R-NT2RM4001569//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//2.0e-35:213:89//AL031663

R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//5.4e-60:558:77//AF071317

R-nnnnnnnnnnnn//M.musculus mRNA of enhancer-trap-locus 1.//4.8e-86:565:85//X69942

R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.083:283:61//U31120

R-NT2RM4001597//HS_2059_A1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence.//4.4e-09:105:83//AQ245136

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//6.7e-111:565:95//AB018334

R-NT2RM4001611//Homarus americanus ryanodine receptor (RyR) mRNA, partial cds.//1.0:364:61//AF051936

R-NT2RM4001629//RPCI11-54G14.TJ RPCI11 Homo sapiens genomic clone R-54G14, genomic survey sequence.//0.0018:347:61//AQ083173

R-NT2RM4001650

R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//0.75:212:62//AL022575

R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//2.6e-26:461:65//AC004685

R-NT2RM4001682//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//1.5e-107:544:96//AL031775

R-NT2RM4001710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//1.8e-110:580:95//AL031447

R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-10:543:59//AC004153

R-nnnnnnnnnnnn//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//8.7e-111:577:94//AL034430

R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF92 locus.//0.017:93:73//M80527

R-NT2RM4001741//Mouse mRNA for talin.//2.4e-34:273:83//X56123

R-NT2RM4001746//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316G12, WORKING DRAFT SEQUENCE.//1.7e-112:567:96//AL031709

R-NT2RM4001754//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.4e-64:475:83//AC002483

R-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//1.
9e-18:202:78//Z83868

R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.
0e-22:236:80//AB018270

R-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//4.4e-1
06:551:95//AC006017

R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, g
enomic survey sequence.//0.76:279:60//B27099

R-NT2RM4001813

R-NT2RM4001823

R-NT2RM4001828//HS_3073_A2_E01_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3073 Col=2 Row=I, genomic survey s
equence.//1.6e-46:255:96//AQ121030

R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence.//9.4e-06:141:6
9//U78024

R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA.//1.5e-06:175:65//A
F019184

R-NT2RM4001842//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 u
nordered pieces.//5.0e-07:332:61//AC005077

R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence.//4
.8e-30:235:85//AF046633

R-nnnnnnnnnnnnn//HS_3244_B1_F10_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey
sequence.//3.0e-40:263:89//AQ252798

R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//5
.0e-119:592:97//Y17711

R-NT2RM4001876//Megastigmus wachtli dinucleotide microsatellite, clone M
WA47CT.//0.13:134:64//AJ001069

R-NT2RM4001880

R-NT2RM4001905//HS_2016_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic survey sequence.//0.0066:264:59//AQ226877

R-NT2RM4001922//HS_2228_B2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic survey sequence.//2.5e-35:205:96//AQ065498

R-NT2RM4001930//Homo sapiens chromosome 17, clone hRPC.34_M_24, complete sequence.//0.26:325:63//AC004562

R-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//2.9e-85:421:98//AC005207

R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162

R-NT2RM4001953//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//1.3e-08:175:70//Z83826

R-NT2RM4001965//CIT-HSP-385N14.TR CIT-HSP Homo sapiens genomic clone 385 N14, genomic survey sequence.//5.7e-69:532:81//B55044

R-nnnnnnnnnnnn//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330

R-NT2RM4001979//Homo sapiens full length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241

R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161

R-NT2RM4001987

R-NT2RM4002013

R-NT2RM4002018

R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBNL H195), complete sequence.//3.6e-42:277:89//AC005353

R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.83:476:57//AC006204

R-NT2RM4002054

R-NT2RM4002062//Human microsomal epoxide hydrolase gene, exons 5 and 6./
/0.11:136:67//U06659

R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503:96//U82267

R-NNNNNNNNNNNN//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:554:68/
/U80742

R-NT2RM4002067//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329A5, WORKING DRAFT SEQUENCE.//7.7e-64:476:81//Z97832

R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758

R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0031:403:57//
AC005504

R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//9.4e-07:322:62//AC000383

R-NNNNNNNNNNNN//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//D12646

R-NT2RM4002128//Human HepG2 partial cDNA, clone hmd2e12m5.//2.0e-26:186:90//D17000

R-NT2RM4002140

R-NT2RM4002145//Homo sapiens full length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247

R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562

R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds.//4.5e-110:560:96//AF084535

R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//8.0e-43:302:85//AC005696

R-NT2RM4002189

R-NT2RM4002194//Human Cosmid g5129g129 from 7q31.3, complete sequence.//
0.29:382:60//AC003960

R-NT2RM4002205//Spiroplasma virus (SpV1-R8A2 B) complete genome.//3.5e-0
5:432:56//X51344

R-NT2RM4002213

R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete se
quence.//0.94:198:61//AC004448

R-NT2RM4002251

R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from 7p13-p14, complete
sequence.//2.3e-58:299:85//AC004837

R-NT2RM4002266//H.sapiens CpG island DNA genomic MseI fragment, clone 17
9f11, forward read cpgl79f11.ft1a.//0.72:97:69//Z57487

R-NT2RM4002278//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 u
nordered pieces.//7.5e-49:405:84//AC005069

R-NT2RM4002281//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 702J19, WORKING DRAFT SEQUENCE.//1.7e-13:168:77//AL033531

R-NT2RM4002287

R-NT2RM4002294//Homo Sapiens Chromosome X clone bWXd171, WORKING DRAFT S
EQUENCE, 1 ordered pieces.//0.98:208:65//AC004676

R-NT2RM4002301//HS_2028_A1_E10_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2028 Col=19 Row=I, genomic survey
sequence.//0.94:321:57//AQ233262

R-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1
-22.3. Contains a pseudogene similar to GPISG20 and other exonucleases).
Contains ESTs, STSSs, GSSs, genomic markers D6S1691 and D6S299 and a ca
repeat polymorphism, complete sequence.//1.9e-35:265:84//AL032822

R-nnnnnnnnnnnnn//Human mRNA for KIAA0319 gene, complete cds.//2.4e-42:569
:68//AB002317

R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:391:59//AC004709

R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//8.6e-121:593:97//AB014549

R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs and STS.//3.8e-44:258:86//Z73417

R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//0.00084:345:60//AC005316

R-NT2RM4002390

R-NT2RM4002409//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411

R-NT2RM4002438

R-NT2RM4002446//Human DNA sequence from clone 360A4 on chromosome 16. Contains ESTs, complete sequence.//2.8e-103:533:95//AL031008

R-NT2RM4002452

R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 321D4 (LANL), complete sequence.//0.99:171:64//AC004034

R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//0.96:94:71//Z92545

R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.9e-102:508:97//AF083255

R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//7.0e-31:172:98//AB014591

R-NT2RM4002493//CIT-HSP-2296C24.TF CIT-HSP Homo sapiens genomic clone 22

96C24, genomic survey sequence.//0.46:182:62//AQ006882
R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds.//7.3e-24:134:99//M84711
R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-11:334:63//AC002368
R-nnnnnnnnnnnnn
R-NT2RM4002532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//3.4e-17:171:79//Z97985
R-NT2RM4002534
R-NT2RM4002567//Homo sapiens chromosome 7 clone UWGC:g1564a040 from 7p14-15, complete sequence.//2.2e-26:181:76//AC005271
R-NT2RM4002571
R-NT2RM4002593//CIT-HSP-2303L15.TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey sequence.//0.034:73:82//AQ015579
R-NT2RM4002623//Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence.//0.0014:670:55//AC005862
R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.00087:251:59//AE001422
R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6q27. Contains EST, STSs and a GSS.//2.7e-37:259:86//Z97205
R-NT2RP2000008//RPCI11-41G16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41G16, genomic survey sequence.//4.1e-25:365:70//AQ029090
R-NT2RP2000027//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//6.0e-05:307:62//AC004098
R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290
R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//5.8e-63:325:96//AF061749
R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing en

hancer element responsible for pigment cell-specific transcription).//0.8
8:210:60//D26163

R-NT2RP2000056//Mus musculus epsilon tyrosine phosphatase cytoplasmic is
oform (Ptpre) mRNA, complete cds.//4.7e-38:377:78//U36758

R-NT2RP2000067//Rat mRNA for growth potentiating factor, complete cds.//
6.0e-10:137:79//D42148

R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169),
complete sequence.//3.1e-76:381:98//AC005754

R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 73 of t
he complete sequence.//2.3e-06:380:60//AE001372

R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, com
plete cds.//3.5e-77:379:97//AF050079

R-NT2RP2000079//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1125A11, WORKING DRAFT SEQUENCE.//6.5e-32:314:78//AL034549

R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//5.
6e-74:378:96//AB018338

R-NT2RP2000091//Homo sapiens clone RG015P03, complete sequence.//9.3e-21
:226:76//AC005048

R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X.//
9.2e-40:278:81//Z68873

R-NT2RP2000098//Human BAC clone RG333F24 from 7q11.2-q21, complete seque
nce.//0.34:132:65//AC004015

R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete
sequence.//3.1e-09:259:67//AC003973

R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//1.8e-
74:386:95//AB018356

R-NT2RP2000120//CITBI-E1-2503M8.TR CITBI-E1 Homo sapiens genomic clone 2
503M8, genomic survey sequence.//5.1e-05:87:77//AQ263909

R-nnnnnnnnnnnnn

R-nnnnnnnnnnnnn//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//4.9e-11:153:69//AC004827

R-NT2RP2000147

R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.0058:261:57//U95626

R-NT2RP2000157//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-119:603:96//AC005924

R-NT2RP2000161//CIT-HSP-2045P7.TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey sequence.//0.89:173:63//B79728

R-NT2RP2000175

R-NT2RP2000183

R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence.//4.3e-39:306:83//AC005325

R-NT2RP2000205//Human DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//7.3e-55:306:94//AC004382

R-NT2RP2000232

R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//7.6e-13:144:75//U88401

R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//9.6e-63:410:86//AC004066

R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8.//1.0:282:58//U58726

R-NT2RP2000257//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.5e-11:163:72//AC004894

R-NT2RP2000258//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.58:442:58//AC004077

R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6 p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSSs, GSSs and genomic marker D6S464, complete sequence.//1.1e-39:292:84//AL009179

R-NT2RP2000274//CIT-HSP-237901.TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey sequence.//6.9e-10:121:81//AQ109409

R-NT2RP2000288

R-NT2RP2000289

R-NT2RP2000297//Homo sapiens full length insert cDNA clone ZB81C03.//7.7e-109:519:99//AF086165

R-NT2RP2000298

R-NT2RP2000310//Homo sapiens p53 induced protein mRNA, partial cds.//1.5e-38:224:93//AF010310

R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//4.3e-113:580:96//AL022398

R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.4e-47:367:77//AC006039

R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.9e-08:494:58//L04272

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.4e-46:262:94//U83981

R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRA

FT SEQUENCE, 6 unordered pieces.//3.0e-07:334:61//AC002993
R-NT2RP2000414//Mouse DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone BAC394, WORKING DRAFT SEQUENCE.//7.0e-08:98:83//AJ004828
R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640_I_15, complet
e sequence.//0.99:150:62//AC005324
R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
complete cds.//4.6e-19:142:90//AF102265
R-NT2RP2000438//RPCI11-62I13.TK RPCI11 Homo sapiens genomic clone R-62I1
3, genomic survey sequence.//3.1e-06:103:79//AQ199572
R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete
sequence.//2.0e-22:276:73//AC004691
R-NT2RP2000459//CIT-HSP-2013N9.TR CIT-HSP Homo sapiens genomic clone 201
3N9, genomic survey sequence.//5.5e-27:205:87//B53940
R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 contain
ing PLZF gene encoding kruppel-like zinc finger protein, complete sequen
ce.//6.0e-12:119:84//AC001234
R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18
) , 5'-flanking region and exon 1.//0.48:201:64//D10170
R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop r
egion, complete sequence.//3.6e-07:472:59//AF033929
R-nnnnnnnnnnnnn
R-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 150C2, WORKING DRAFT SEQUENCE.//2.3e-61:317:97//AL022318
R-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds./
/6.6e-29:167:97//AB005543
R-NT2RP2000617
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//2.
5e-64:335:96//AB014514
R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Co

ntains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSS. Contains polymorphic CA repeat.//1.8e-28:383:70//Z92545

R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSS and GSSs, complete sequence.//0.0093:110:70//AL021997

R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds.//0.73:301:60//U89796

R-NT2RP2000668

R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE.//2.8e-11:256:66//AP000015

R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.036:176:69//AC002346

R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//2.7e-110:555:96//AC004540

R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSS and GSSs, and a ca repeat polymorphism, complete sequence.//2.6e-18:319:68//AL023775

R-NT2RP2000758//CIT-HSP-507A14.TP CIT-HSP Homo sapiens genomic clone 507A14, genomic survey sequence.//1.0:189:60//B50590

R-NT2RP2000764

R-NT2RP2000809//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-24:215:81//AC004002

R-NT2RP2000812//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//9.5e-32:176:97//B99575

R-nnnnnnnnnnnnn//paramecium species 5,87 mt dna dimer: replication init.

region.//0.0077:418:57//K00916

R-NT2RP2000816//F.rubripes GSS sequence, clone 011H02aA6, genomic survey
sequence.//0.61:52:73//AL011013

R-NT2RP2000819

R-NT2RP2000841//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 43408, WORKING DRAFT SEQUENCE.//0.00012:181:70//AL033504

R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA fro
m renin-expressing kidney tumor cell line, partial sequence.//3.7e-27:38
8:72//U13370

R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849_N_15, complet
e sequence.//0.0022:200:68//AC005703

R-NT2RP2000863

R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, part
ial.//2.3e-43:279:89//AJ006412

R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat e
pithelium cancer , segment 7/10.//0.0028:221:62//AB020875

R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2
.2e-55:290:96//AB018266

R-NT2RP2000938//Homo sapiens full length insert cDNA clone ZD55G12.//2.1
e-37:215:93//AF086336

R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3
.0e-96:494:96//AB018298

R-NT2RP2000965

R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 2
2q12.1. Contains ESTs, STSS and GSSs and genomic marker D22S56, complete
sequence.//4.5e-87:440:97//AL021393

R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M_12, complet
e sequence.//5.4e-93:484:95//AC005277

R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of t

he complete sequence.//2.1e-06:318:62//AE001372

R-NT2RP2001036//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//2.0e-24:273:73//AL031732

R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140

R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029

R-NT2RP2001070//CITBI-E1-2503F4.TF CITBI-E1 Homo sapiens genomic clone 2503F4, genomic survey sequence.//0.13:97:72//AQ265973

R-NT2RP2001094//Mycoplasma mycoides mycoides SC immunodominant protein P72 (p72) gene, complete cds, mannitol-1-phosphate dehydrogenase (mt1D) gene, partial cds and insertion sequence IS1296, complete sequence.//0.018:373:57//U61140

R-NT2RP2001119

R-NT2RP2001127//Homo sapiens HRIHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348

R-NT2RP2001137//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394

R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//I01838

R-NT2RP2001168

R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB007949

R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey sequence.//1.3e-33:204:93//B89680

R-NT2RP2001196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence.//1.7e-06:413:61//AL010134

R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//8.5e-15:278:68//AL022153

R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP-associated Cyclophilin (U SA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.//0.0020:462:57//AL030995

R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 2356P23, genomic survey sequence.//8.0e-108:547:96//AQ081110

R-NT2RP2001245//Spodoptera frugiperda 16S rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein gene, 5' end.//0.0052:350:58//M76713

R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//4.6e-111:544:97//AB018353

R-NT2RP2001277//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS ** * from clone Y59A8, WORKING DRAFT SEQUENCE.//0.0058:327:59//Z98870

R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:187:65//AC004709

R-NT2RP2001295//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//0.59:218:62//AC006041

R-NT2RP2001312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.12:117:64//AL033520

R-NT2RP2001327//Caenorhabditis elegans cosmid R04D3, complete sequence.//0.31:119:66//Z70212

R-NT2RP2001328//HS_2213_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=13 Row=G, genomic survey

sequence.//1.7e-22:200:83//AQ136874

R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence.//0.81:5
09:56//AL034560

R-NT2RP2001378//H.sapiens DNA sequence.//0.94:147:63//Z22404

R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds.//3.2e-09:75:9
7//AF091433

R-NT2RP2001392//Myxococcus xanthus ATP-dependent protease (bsgA) gene, c
omplete cds.//0.079:178:62//L19301

R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X conta
ins ESTs STS, CpG islands and polymorphic CA repeat.//3.4e-60:351:90//Z9
3242

R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds.//5.4e-55:320:83
//D17294

R-NT2RP2001420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1108D11, WORKING DRAFT SEQUENCE.//1.0e-44:246:85//AL034419

R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36.
11-36.23. Contains ESTs and a GSS, complete sequence.//3.7e-05:417:61//A
L031273

R-NT2RP2001427//Human Chromosome 11 Cosmid cSRL34e5, complete sequence./
/0.94:287:59//U73643

R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//5.
2e-31:299:77//AF046702

R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-subtype,
complete cds.//7.8e-75:548:83//D17447

R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Canc
er Institute Human PAC Library) complete sequence.//1.0e-06:452:59//AC00
4801

R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21
unordered pieces.//5.1e-08:218:67//AC004846

R-NT2RP2001450

R-NT2RP2001467//Human BAC clone RG343P13 from 7q31, complete sequence.//
3.8e-31:254:83//AC002465

R-NT2RP2001506//C.barati p-47, ntnh, bonT genes.//1.2e-06:415:60//Y12091

R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence.//0.11:1
55:63//AL034559

R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL
AR1.//2.1e-104:545:95//Y14494

R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete
sequence.//7.0e-16:283:68//AC004596

R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containing
XRCC3 DNA repair gene, genomic sequence, complete sequence.//7.7e-16:108
:96//AF037222

R-NT2RP2001560//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A
-56H4, genomic survey sequence.//0.052:112:66//B73597

R-NT2RP2001569//CIT-HSP-2335F8.TF CIT-HSP Homo sapiens genomic clone 233
5F8, genomic survey sequence.//6.0e-78:383:98//AQ042029

R-NT2RP2001576//Homo sapiens sulfonylurea receptor (SUR2) gene, exon 37.
//0.33:135:66//AF061322

R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer.//2.7e-07:240:63/
/L15407

R-NT2RP2001597//HS_3016_B2_F06_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3016 Col=12 Row=L, genomic survey
sequence.//5.3e-45:310:87//AQ118854

R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855_D_21, complet
e sequence.//0.015:445:58//AC006079

R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene,
complete sequence.//3.5e-16:413:63//AF009326

R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal prot

ein S12 (G6) edited mRNA, complete cds.//0.11:190:63//AF034626
R-NT2RP2001663//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//3.0e-26:157:81//AC004125
R-NT2RP2001677//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.0e-58:305:96//AC004472
R-NT2RP2001678//Human BAC clone RG222A16 from 7q31, complete sequence.//0.95:107:66//AC002385
R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternatively spliced erythroid ankyrins (Ank1) gene, putative exon 41 and partial cds.//8.8e-05:211:63//U76758
R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.7e-68:352:97//AC004079
R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=11 Row=N, genomic survey sequence.//7.7e-05:346:59//B40914
R-NT2RP2001740//HS_3213_A2_D02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//1.1e-16:162:82//AQ175104
R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds.//2.0e-33:312:77//D16583
R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//2.3e-100:435:97//AC004783
R-NT2RP2001813//Human leukocyte common antigen T200 (CD45, LCA) gene, exon 9.//0.031:261:60//M23468
R-NT2RP2001861
R-NT2RP2001869//Sequence 5 from patent US 5595900.//4.2e-21:194:77//I34189
R-NT2RP2001876
R-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-

25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.0e-111:485:97//AL031864

R-NT2RP2001900

R-NT2RP2001907//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//5.4e-42:382:77//U07563

R-NT2RP2001926//HS_3180_B2_F02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=L, genomic survey sequence.//2.8e-25:138:80//AQ185415

R-NT2RP2001936//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:60//AC005504

R-NT2RP2001943//Dictyostelium discoideum PkgA (pkgA) gene, partial cds.//1.4e-08:378:59//AF020280

R-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.6e-85:409:100//AC005033

R-NT2RP2001947//Human mRNA for KIAA0390 gene, complete cds.//0.85:140:64//AB002388

R-NT2RP2001969

R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//2.0e-60:307:98//B99575

R-NT2RP2001985//Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project).//0.031:282:61//AL022140

R-NT2RP2002025

R-NT2RP2002032//CITBI-E1-2502C19.TF CITBI-E1 Homo sapiens genomic clone 2502C19, genomic survey sequence.//1.2e-52:285:95//AQ264715

R-NT2RP2002033//Human (lambda) DNA for immunoglobulin light chain.//1.1e-08:389:61//D88270

R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPCI11-319E16 (Roswell Park Can

cer Institute Human BAC Library) complete sequence.//1.1e-49:264:97//AC006206

R-NT2RP2002046//Human BAC clone GS119P05 from 7q21, complete sequence.//0.0023:429:61//AC004011

R-NT2RP2002047//P.falciparum PK1 gene.//0.00015:239:62//X83707

R-NT2RP2002058//HS_2183_A1_G01_MR CIT Approved Human Genomic Spermlibrary D Homo sapiens genomic clone Plate=2183 Col=1 Row=M, genomic survey sequence.//1.2e-21:185:84//AQ022560

R-NT2RP2002066//G.gallus microsatellite DNA (LEI0222 (=T15ivD04)).//0.18:102:70//Z83792

R-NT2RP2002070//P.falciparum major merozoite surface antigen (PMMSA) mRNA, complete cds, isolate FC27.//0.95:192:61//M19143

R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//3.8e-25:182:86//AF052183

R-NT2RP2002079//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LC B-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//1.7e-10:97:90//AL009178

R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//4.6e-59:376:89//AJ007509

R-NT2RP2002105

R-NT2RP2002124//RPCI11-75J16.TJ RPCI11 Homo sapiens genomic clone R-75J16, genomic survey sequence.//0.58:191:64//AQ266779

R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//0.0065:294:61//AC005913

R-NT2RP2002154

R-NT2RP2002172//RPCI11-90C20.TJ RPCI11 Homo sapiens genomic clone R-90C20, genomic survey sequence.//0.049:160:65//AQ282591

R-NT2RP2002185//CIT-HSP-2341I15.TF CIT-HSP Homo sapiens genomic clone 2341I15, genomic survey sequence.//6.0e-36:230:90//AQ053355

R-NT2RP2002192//HS_2222_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=15 Row=L, genomic survey sequence.//1.9e-15:249:71//AQ178491

R-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//4.7e-35:438:73//AF032872

R-NT2RP2002208//Hansenula wingei mitochondrial DNA, complete sequence.//0.00057:468:57//D31785

R-NT2RP2002219//HS_2058_A1_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=E, genomic survey sequence.//3.4e-55:512:77//AQ234380

R-NT2RP2002231//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-31, complete sequence.//1.5e-06:398:61//Z98557

R-nnnnnnnnnnnn//Sequence 11 from patent US 5624818.//3.3e-91:553:87//I41141

R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//3.0e-14:132:84//AF005418

R-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//1.6e-96:548:91//AL033527

R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.1e-06:391:60//AC004605

R-NT2RP2002292//Genomic sequence from Human 13, complete sequence.//0.91:159:64//AC001226

R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.3e-101:527:94//AF069532

R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of

the complete sequence.//0.00052:389:59//AE001408

R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds.//2.3e-112:567:95//AF093668

R-NT2RP2002333//Rat POU domain factor (Brn-5) mRNA.//1.5e-22:323:73//L23204

R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//3.7e-102:600:89//AF038958

R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:399:59//AC005308

R-NT2RP2002408//HS_2212_A1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=I, genomic survey sequence.//9.6e-35:231:88//AQ184632

R-NT2RP2002426//Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.//2.8e-39:308:82//AL021877

R-NT2RP2002439//Leishmania tarentolae mitochondrial electron transport chain component mRNA.//0.022:102:71//M74225

R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.00099:354:59//Z99289

R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE.//0.0015:219:67//AP000013

R-NT2RP2002475

R-nnnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//3.1e-113:605:92//AB005289

R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//0.32:210:64//Z98047

R-NT2RP2002503//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.0e-86:429:98//AC006213

R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//2.7e-105:583:91//AB018334

R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//0.14:406:58//AJ223323

R-NT2RP2002537//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 500L14, WORKING DRAFT SEQUENCE.//2.8e-16:188:78//AL023583

R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA.//4.7e-108:571:93//AF009314

R-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//1.1e-103:422:95//AC005316

R-NT2RP2002591//Human DNA binding protein (HPF2) mRNA, complete cds.//1.8e-36:526:67//M27878

R-NT2RP2002595

R-NT2RP2002606//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.//7.2e-10:211:71//AL033529

R-NT2RP2002609

R-NT2RP2002618//Plasmodium falciparum MAL3P6, complete sequence.//2.9e-05:566:60//Z98551

R-NT2RP2002621//Human DNA sequence from PAC 341I10 on chromosome 6q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo)gene, ESTs and STSs.//1.1e-38:348:78//Z97352

R-NT2RP2002643//Homo sapiens chromosome 11 clone pTWB15.28 map 11p15.4-p15.5, genomic survey sequence.//1.2e-35:414:66//AF074030

R-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//1.3e-77:403:95//AC005384

R-NT2RP2002701

R-NT2RP2002706//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.0e-42:147:90//AC005778

R-NT2RP2002710//P.falciparum serine rich protein (SERP I) gene.//0.84:135:67//J03983

R-NT2RP2002727//, complete sequence.//1.0:363:59//AC005815

R-NT2RP2002736//Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence.//0.44:267:60//AC004138

R-NT2RP2002740//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//0.0016:474:60//AC004674

R-NT2RP2002741//HS_3051_B1_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=21 Row=P, genomic survey sequence.//1.1e-38:217:86//AQ106283

R-NT2RP2002750//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.0e-36:430:75//AC002395

R-NT2RP2002752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 366L4, WORKING DRAFT SEQUENCE.//8.2e-41:437:76//AL023494

R-NT2RP2002753//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-100:496:97//AC004882

R-NT2RP2002769//paramecium species 5,311 mt dna dimer: replication init. region.//7.4e-10:404:60//K00917

R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence.//1.2e-63:341:94//AF070537

R-NT2RP2002800//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-1

1-37G8, genomic survey sequence.//4.9e-60:321:95//AQ029850
R-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.9e-100:492:98//AC006078
R-NT2RP2002857//HS_3026_B2_H07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=14 Row=P, genomic survey sequence.//8.9e-06:242:62//AQ128697
R-NT2RP2002862//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I15, genomic survey sequence.//1.5e-44:270:85//AQ052700
R-NT2RP2002880//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.0:295:58//AL022318
R-NT2RP2002891
R-NT2RP2002925//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 243L18, WORKING DRAFT SEQUENCE.//2.0e-24:395:67//AL034395
R-NT2RP2002928//Plasmodium falciparum MAL3P5, complete sequence.//0.044:461:55//AL034556
R-NT2RP2002929//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.35:491:56//AC005140
R-NT2RP2002954//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//1.0:275:61//AC005701
R-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//2.7e-61:508:79//U62483
R-NT2RP2002979//RPCI11-20F13.TPK RPCI-11 Homo sapiens genomic clone RPCI-11-20F13, genomic survey sequence.//0.88:110:72//AQ008132
R-NT2RP2002980//Homo sapiens PAC clone DJ0841B21 from 7q21.1-q31.1, complete sequence.//1.1e-102:433:95//AC004140
R-NT2RP2002986//Human DNA sequence from clone 1147016 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains

an STS and GSSs, complete sequence.//0.31:219:62//AL031542

R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence.//1.3e-51:283:88//AC005968

R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21.//4.3e-11:430:63//AL021307

R-NT2RP2003000//Saccharomyces cerevisiae mitochondrion transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.//0.00088:347:62//L36887

R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 2/10.//3.5e-33:271:82//AB020870

R-NT2RP2003073

R-NT2RP2003099//Homo sapiens PAC clone DJ0886008 from 7q32-q35, complete sequence.//1.5e-45:548:69//AC004914

R-NT2RP2003108

R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-51:323:88//AC005378

R-NT2RP2003121//HS_2238_A1_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=I, genomic survey sequence.//0.00055:324:61//AQ293058

R-NT2RP2003125

R-NT2RP2003129

R-NT2RP2003137//Human BAC clone RG084D04 from 7q31, complete sequence.//1.1e-46:521:74//AC003084

R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence.//1.0:368:59//AC005879

R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR.//1.0:120:64//M25581

R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPK.1018_N_14, complete sequence.//2.2e-71:467:86//AC005823

R-NT2RP2003177

R-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996D20, WORKING DRAFT SEQUENCE.//1.1e-95:585:88//AL031597

R-NT2RP2003206//P.falciparum interspersed repeat antigen (FIRA) gene.//0.039:338:60//M17877

R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-11:542:60//Z98551

R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MDH9, complete sequence.//1.0:311:60//AB016888

R-NT2RP2003243//CIT-HSP-2368D12.TR CIT-HSP Homo sapiens genomic clone 2368D12, genomic survey sequence.//0.39:112:66//AQ077738

R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//1.3e-38:273:83//L38481

R-NT2RP2003272//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//4.4e-15:181:66//AC004187

R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//4.2e-110:565:95//AB014525

R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.2e-12:221:70//AC005831

R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//0.86:379:60//AC005261

R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0e-39:418:74//AC005079

R-NT2RP2003295//HS_2053_B1_A10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence.//0.0016:346:61//AQ235251

R-NT2RP2003297//Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence.//0.74:397:56//AC002332

R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence.//0.99:447:60//AC004960

R-NT2RP2003329//C.reinhardtii psbB 5' flanking region.//0.79:161:59//X59731

R-NT2RP2003339//RPCI11-57H15.TK RPCI11 Homo sapiens genomic clone R-57H15, genomic survey sequence.//0.13:184:64//AQ116039

R-NT2RP2003347//RPCI11-15B19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15B19, genomic survey sequence.//6.4e-31:218:89//B76357

R-NT2RP2003367//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//9.0e-11:101:84//U91321

R-NT2RP2003391//HS_2255_B2_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937

R-NT2RP2003393//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//3.9e-31:290:79//AQ202481

R-NT2RP2003394//Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I.//5.1e-14:579:61//X14910

R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, partial cds.//0.32:174:66//U81429

R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536

R-NT2RP2003445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//4.4e-99:585:89//AL023808

R-NT2RP2003446

R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559

R-NT2RP2003480//Homo sapiens full length insert cDNA clone ZE09A11.//4.7e-111:540:98//AF086540

R-NT2RP2003499

R-NT2RP2003506

R-NT2RP2003511

R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566
:93//D87460

R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2)
mRNA, complete cds.//1.5e-60:518:79//M12783

R-NT2RP2003522//HS_2182_A1_D05_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2182 Col=9 Row=G, genomic survey s
equence.//0.053:251:60//AQ024304

R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKI
NG DRAFT SEQUENCE, 31 unordered pieces.//1.5e-37:328:80//AC005841

R-NT2RP2003543//HS_3028_A2_C12_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3028 Col=24 Row=E, genomic survey
sequence.//2.0e-39:203:100//AQ094957

R-NT2RP2003559//Homo sapiens full length insert cDNA clone ZD65E09.//2.3
e-59:325:95//AF088055

R-NT2RP2003564

R-NT2RP2003581

R-NT2RP2003596//HS_2163_B1_D11_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2163 Col=21 Row=H, genomic survey
sequence.//0.0011:212:67//AQ125143

R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete c
ds.//5.4e-102:501:97//U97067

R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 geno
mic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0012:363:61
//AC005507

R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthe
tase.//5.1e-37:561:68//AJ006215

R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS67

91 and DXS8038 on chromosome X contains ESTs.//0.0053:395:58//Z76735

R-NT2RP2003687//Human BAC clone RG222A16 from 7q31, complete sequence.//8.0e-10:205:67//AC002385

R-NT2RP2003691//HS_3252_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=22 Row=A, genomic survey sequence.//5.3e-05:332:60//AQ219783

R-NT2RP2003702//CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey sequence.//3.9e-43:431:75//AQ035000

R-NT2RP2003704

R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-45:265:93//AB011097

R-NT2RP2003713//Human DNA sequence from PAC 411B6 on chromosome X *.//0.64:169:67//Z84470

R-NT2RP2003714//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.//4.6e-11:152:73//Z95704

R-NNNNNNNNNNNN//H.sapiens mRNA for PIBF1 protein, complete.//0.94:443:59//Y09631

R-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.2e-109:547:96//AC004951

R-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//4.1e-109:545:97//AC004626

R-NT2RP2003760//B. taurus mRNA for gamma-COP.//6.3e-28:400:69//X70019

R-NT2RP2003764//Mouse preprosomatostatin gene.//0.90:285:62//X51468

R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development, complete cds.//0.96:446:58//D87956

R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds.//1.8e-104:531:96//AF047437

R-NT2RP2003777

R-NT2RP2003781//HS 3109 B1 B04 T7 CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey s
equence.//1.3e-60:346:92//AQ186749

R-NT2RP2003793

R-NT2RP2003840

R-NT2RP2003857//HS_2205_A2_H12_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2205 Col=24 Row=0, genomic survey
sequence.//8.1e-22:127:99//AQ151299

R-NT2RP2003859//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-1
1-37G8, genomic survey sequence.//8.3e-60:320:95//AQ029850

R-NT2RP2003871//HS_3210_A1_C08_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic survey
sequence.//8.6e-09:322:61//AQ175028

R-NT2RP2003885//RPCI11-7M10.TP RPCI-11 Homo sapiens genomic clone RPCI-1
1-7M10, genomic survey sequence.//4.7e-67:380:92//B72214

R-NT2RP2003912//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 32B1, WORKING DRAFT SEQUENCE.//1.2e-33:379:75//AL023693

R-NT2RP2003952

R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease,
complete cds.//2.3e-114:568:97//AB014458

R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//1
.1e-107:540:97//AB007916

R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//7.
7e-114:568:96//AB018347

R-NT2RP2003984

R-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENC
E, 11 unordered pieces.//6.6e-99:551:92//AC000382

R-NT2RP2003988

R-NT2RP2004014

R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequ

ence.//4.9e-114:568:97//AC004780

R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library *Oryza sativa* genomic clone nbxb0020F03r, genomic survey sequence.//0.11:195:64//AQ258389

R-nnnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//7.6e-110:564:95//AL034555

R-NT2RP2004081//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:503:57//AC005308

R-NT2RP2004098//*H.sapiens* CpG island DNA genomic MseI fragment, clone 133h3, reverse read cpg133h3.rt1a.//7.9e-25:140:100//Z64530

R-NT2RP2004124

R-NT2RP2004142//CIT-HSP-2316F21.TR CIT-HSP *Homo sapiens* genomic clone 2316F21, genomic survey sequence.//2.8e-83:409:98//AQ034964

R-NT2RP2004152//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776

R-NT2RP2004165//*Anthocidaris crassispina* mRNA for dynein beta-heavy chain, complete cds.//3.4e-20:343:65//D01021

R-NT2RP2004170//*** SEQUENCING IN PROGRESS *** *Homo sapiens* chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-89:587:86//AC004064

R-NT2RP2004172//*Dictyostelium discoideum* LTR-retrotransposon Skipper, partial genomic sequence, 3' end.//0.24:440:60//AF017047

R-NT2RP2004187//RPCI11-59E12.TK RPCI11 *Homo sapiens* genomic clone R-59E12, genomic survey sequence.//3.1e-05:175:66//AQ198120

R-NT2RP2004194

R-NT2RP2004196//*Fugu rubripes* GSS sequence, clone 076D01bE2, genomic survey sequence.//1.6e-22:178:71//AL026601

R-NT2RP2004207//*Homo sapiens* BAC clone GS421I03 from Xq25-q26, complete

sequence.//0.19:175:64//AC005023

R-NT2RP2004226//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone Y313F4, WORKING DRAFT SEQUENCE.//6.1e-17:445:64//AL023808

R-NT2RP2004232//M.musculus (Balb/c) mRNA for serine/threonine protein ki
nase.//3.2e-25:326:71//Z34524

R-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds./
/8.7e-108:563:94//AB015718

R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cd
s.//1.1e-101:530:93//AF039687

R-NT2RP2004242

R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome
Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphi
sm, STSs and GSSs, complete sequence.//5.1e-08:236:65//AL023280

R-NT2RP2004270//Lycopersicon esculentum ldh2 gene.//0.98:259:61//Y10603

R-NT2RP2004300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913

R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete c
ds.//1.5e-108:544:96//AF000416

R-NT2RP2004321//Caenorhabditis elegans cosmid F47B8, complete sequence./
/0.0078:333:61//Z77662

R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete
sequence.//1.4e-75:306:86//AC005229

R-NT2RP2004347//RPCI11-90N11.TJ RPCI11 Homo sapiens genomic clone R-90N1
1, genomic survey sequence.//2.9e-87:494:92//AQ284548

R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.
1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ES
Ts, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010

R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of
the complete sequence.//3.6e-08:483:57//AE001433

R-NT2RP2004366//F.rubripes GSS sequence, clone 013B16aF3, genomic survey sequence.//2.1e-05:128:67//AL000528

R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065

R-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969

R-NT2RP2004392//Ceratovacuna sp. mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993

R-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//6.4e-11:572:96//AC005164

R-NT2RP2004399//Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.//0.13:253:64//AC006085

R-NT2RP2004400//HS_3238_A2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=22 Row=0, genomic survey sequence.//5.1e-23:162:89//AQ211412

R-NT2RP2004412//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//2.6e-09:458:60//M97514

R-NT2RP2004425//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718

R-NT2RP2004476//Rattus norvegicus activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3' UTR.//5.3e-99:600:90//AF030091

R-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//3.9e-11:575:97//AC005591

R-NT2RP2004512//Plasmodium falciparum MAL3P3, complete sequence.//0.0003
4:517:58//Z98547

R-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//1.8e-1
15:571:97//AC004890

R-NT2RP2004538//Homo sapiens BAC clone RG318C11 from 7p14-p15, complete
sequence.//1.7e-47:322:87//AC005091

R-NT2RP2004551//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Sys
tems Human BAC Library) complete sequence.//0.035:511:58//AC005184

R-NT2RP2004568//T7C20-Sp6 TAMU Arabidopsis thaliana genomic clone T7C20,
genomic survey sequence.//0.70:446:54//B08766

R-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768

R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP Homo sapiens genomic clone 23
76P22, genomic survey sequence.//0.0079:223:63//AQ108976

R-NT2RP2004594//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, c
omplete sequence.//5.3e-10:493:62//AC004605

R-NT2RP2004600//Homo sapiens full length insert cDNA clone ZE04E06.//2.1
e-70:343:99//AF086522

R-NT2RP2004602//Homo sapiens full length insert cDNA clone YW26E09.//2.0
e-96:528:93//AF086033

R-NT2RP2004614

R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//7.3e-117:58
7:96//AJ006291

R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.
8e-105:520:96//AB007929

R-NT2RP2004675//Human elastin (ELN) gene, partial cds, and LIM-kinase (L
IMK1) gene, complete cds.//3.4e-22:197:79//U63721

R-NT2RP2004681//Rat notch 2 mRNA.//8.0e-30:276:78//M93661

R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.

6e-118:600:96//AB014525

R-NT2RP2004709//Homo sapiens full length insert cDNA clone ZD42A08.//3.5
e-14:139:86//AF086259

R-NT2RP2004710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 126A5, WORKING DRAFT SEQUENCE.//6.9e-117:592:96//AL031447

R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//4
.2e-117:594:96//AB007947

R-NT2RP2004743//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.53:403:59//AC0
05505

R-NT2RP2004767//Human DNA sequence from PAC 491M17 on chromosome 1p36.2-
1p36.3.//2.0e-81:568:84//Z97988

R-NT2RP2004775//Anopheles quadrimaculatus NADH dehydrogenase subunits (1
-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatas
e subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and s
mall subunits).//4.0e-08:365:62//L04272

R-NT2RP2004791//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192),
complete sequence.//7.8e-111:541:98//AC005216

R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta s
ubunit (SCS) mRNA, partial cds.//2.5e-114:564:96//AF058953

R-NT2RP2004802

R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.7e
-118:584:97//AF054179

R-NT2RP2004841//Human BAC clone RG308B22 from 7q22-q31, complete sequenc
e.//4.0e-46:447:72//AC002089

R-NT2RP2004861//Plasmodium falciparum MAL3P5, complete sequence.//0.19:1
89:66//AL034556

R-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence.//1.
1e-08:330:61//AC004383

R-NT2RP2004936//CIT-HSP-2374L4.TF CIT-HSP Homo sapiens genomic clone 237
4L4, genomic survey sequence.//0.99:129:65//AQ110571
R-nnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.014:
402:61//Z98551
R-NT2RP2004961//RPCI11-45P2.TK RPCI11 Homo sapiens genomic clone R-45P2,
genomic survey sequence.//9.3e-90:453:97//AQ202282
R-NT2RP2004962//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y40H4, WORKING DRAFT SEQUENCE.//0.017:291:61//AL022573
R-NT2RP2004967//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 u
nordered pieces.//4.6e-52:496:77//AC005077
R-NT2RP2004978//Homo sapiens chromosome 19, cosmid F23269, complete sequ
ence.//0.088:322:63//AC005614
R-NT2RP2004982//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, compl
ete sequence.//0.025:339:61//AC003071
R-NT2RP2004985//T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24,
genomic survey sequence.//0.40:111:70//B78148
R-NT2RP2004999//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30
unordered pieces.//0.23:157:68//AC005682
R-NT2RP2005000
R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//3
.0e-111:577:95//AB014515
R-NT2RP2005003//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome System
s Human BAC library) complete sequence.//2.4e-21:246:77//AC004673
R-nnnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//9.5e-115
:568:97//AF100141
R-NT2RP2005018//HS_3108_B1_E09_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3108 Col=17 Row=J, genomic survey
sequence.//1.9e-31:222:89//AQ104050
R-NT2RP2005020//Rattus norvegicus cationic amino acid transporter-1 (CAT

-1) mRNA, complete cds.//6.6e-41:566:73//U70476
R-NT2RP2005031//CIT-HSP-516A2.TV CIT-HSP Homo sapiens genomic clone 516A
2, genomic survey sequence.//4.1e-31:357:75//B49897
R-NT2RP2005037
R-NT2RP2005038//Sequence 5 from patent US 5552281.//2.2e-32:178:98//I256
44
R-NT2RP2005108//Mus musculus orphan nuclear hormone receptor (CAR) gene,
complete sequence.//3.7e-23:475:67//AF009326
R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//8.
4e-104:518:97//AB014564
R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box
protein).//1.4e-67:464:85//X98743
R-NT2RP2005139
R-NT2RP2005140//Leishmania mexicana amazonensis kinetoplast (clone 29) m
axicircle A+T-rich repetitive DNA sequence.//7.9e-08:460:60//U00101
R-NT2RP2005144//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORK
ING DRAFT SEQUENCE, 129 ordered pieces.//2.5e-103:519:96//AC005911
R-NT2RP2005147//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21
unordered pieces.//0.068:100:75//AC004971
R-NT2RP2005159//CITBI-E1-2506A8.TF CITBI-E1 Homo sapiens genomic clone 2
506A8, genomic survey sequence.//0.90:113:71//AQ262104
R-NT2RP2005162//Homo sapiens chromosome 17, clone HCIT307A16, complete s
equence.//5.0e-14:183:75//AC003041
R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.5
e-100:513:95//AJ007509
R-NT2RP2005204
R-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete
sequence.//7.2e-119:583:97//AC005189
R-NT2RP2005239//Homo sapiens mRNA for putative tRNA splicing protein, pa

rtial.//8.4e-62:312:98//AJ010952

R-NT2RP2005254//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//5.7e-09:328:62//Z99297

R-NT2RP2005270//Plasmodium falciparum MAL3P8, complete sequence.//2.3e-05:355:61//AL034560

R-NT2RP2005276//Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence.//0.0014:541:58//AC000107

R-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//4.4e-69:459:86//L26335

R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.4e-124:594:98//AF060219

R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//1.5e-110:545:96//AJ007590

R-NT2RP2005293//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//1.1e-12:554:61//U00101

R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//9.5e-15:218:77//AL022069

R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence.//2.0e-72:478:88//L06804

R-NT2RP2005336//***ALU WARNING: Human Alu-J subfamily consensus sequence.//7.3e-33:139:82//U14567

R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.//0.094:451:60//Z97629

R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-11:89:96//AJ010841

R-NT2RP2005360//Homo sapiens clone RG023I15, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.046:266:60//AC005049

R-NT2RP2005393//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//6.0e-41:226:86//AC005695

R-NT2RP2005407

R-NT2RP2005436//Polistes annularis (clone pan117AAT) tandem repeat region.//0.039:169:63//L10835

R-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//3.0e-38:263:88//AQ055548

R-NT2RP2005453//CIT-HSP-2367N1.TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey sequence.//0.67:409:59//AQ079845

R-NT2RP2005457//Homo sapiens partial XPGC gene, exon 2.//2.0e-42:315:82//X71342

R-NT2RP2005464//CIT-HSP-2359C16.TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey sequence.//1.0:251:60//AQ075816

R-NT2RP2005465//Drosophila melanogaster, chromosome 2R, region 44D1-44D2, P1 clone DS08616, complete sequence.//0.25:288:62//AC005457

R-NT2RP2005472//Chlorarachnion CCMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE), ATP-dependent clp protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA POLII), and RNA helicase homolog (RNAHEL) genes, complete cds.//1.0:356:59//U58510

R-NT2RP2005476//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//0.00092:421:60//AL031746

R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.2e-71:187:100//AC006030

R-NT2RP2005491//paramecium species 5,311 mt dna dimer: replication init. region.//1.6e-10:403:62//K00917

R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.3e-25:208:82//AC005051

R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSS, GSSs and two CA repeat polymorphisms, complete sequence.//1.5e-22:196:84//AL022722

R-NT2RP2005498

R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//1.7e-29:252:76//AC005828

R-NT2RP2005509//CIT-HSP-2060J6.TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey sequence.//3.1e-53:402:84//B69979

R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//9.9e-109:570:94//AF092563

R-NT2RP2005525//Human clone JkA2 mRNA induced upon T-cell activation, 3' end.//5.1e-32:175:98//U38432

R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence.//0.94:288:61//AC004911

R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.7e-106:560:94//AJ012449

R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.3e-114:583:96//AB007963

R-NT2RP2005549//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//0.91:287:58//AJ011929

R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Canc

er Institute Human PAC library) complete sequence.//3.6e-05:222:66//AC004804

R-NT2RP2005557//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//8.2e-22:236:76//AC004996

R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.2e-45:286:85//AC006146

R-NT2RP2005600//Human polymorphic microsatellite DNA.//0.043:304:58//M99148

R-NT2RP2005605//Human Cosmid g1572c190, complete sequence.//2.4e-17:163:77//AC000126

R-NT2RP2005620

R-NT2RP2005622//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.010:308:58//B13538

R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72//AC005996

R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Scca2) gene, complete cds.//0.030:370:60//AF063937

R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08:355:62//AE001398

R-NT2RP2005651

R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908

R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//6.7e-117:594:95//AF069984

R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//1.8e-89:434:98//AF089814

R-NT2RP2005683//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.037:283:58//B135

38

R-NT2RP2005690//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:295:83//AC005478

R-NT2RP2005694//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-106, complete sequence.//0.0026:414:57//AL010210

R-NT2RP2005701

R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342

R-NT2RP2005719//Caenorhabditis elegans cosmid LLC1, complete sequence.//0.83:275:61//Z82277

R-NT2RP2005722//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985

R-NT2RP2005723

R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-64:503:82//AC004842

R-NT2RP2005741//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.5e-09:261:64//AC000384

R-NT2RP2005748//RPCI11-64K11.TK RPCI11 Homo sapiens genomic clone R-64K11, genomic survey sequence.//0.00039:215:66//AQ239313

R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868

R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516

R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6 p24.1-p25.3.//9.7e-34:172:86//AL022098

R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672

R-NT2RP2005773//HS_2168_B1_G12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414

R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:59
1:88//D13310

R-NT2RP2005781//Streptomyces sp. genomic DNA for sarcosine oxidase.//0.0
19:384:59//D10623

R-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423

R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPK.147_L_13, complet
e sequence.//6.3e-16:481:63//AC005332

R-NT2RP2005812//Caenorhabditis elegans cosmid F15B10.//0.81:147:63//AF03
6696

R-NT2RP2005815

R-NT2RP2005835

R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//
1.5e-26:512:64//Z68873

R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. C
ontains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047

R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. C
ontains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308

R-NT2RP2005859//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from contig 3-83, complete sequence.//0.0097:363:59//AL010152

R-NT2RP2005868//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971

R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:6
7//L11316

R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from base
s 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence
.//0.89:276:60//AE000661

R-NT2RP2005908

R-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//1

.2e-40:285:80//U63840

R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6 q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSS and genomic marker D6S416, complete sequence.//0.0011:480:58//Z99289

R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//8.9e-21:136:78//AC004616

R-NT2RP2006023//HS_2176_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence.//2.5e-66:369:95//AQ023148

R-NT2RP2006038//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.00029:408:58//AE001369

R-NT2RP2006043//Polistes annularis (clone pan117AAT) tandem repeat region.//0.032:195:62//L10835

R-NT2RP2006052//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.11:263:61//AC005140

R-NT2RP2006069

R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00044:333:61//AC004709

R-NT2RP2006098//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-77, complete sequence.//4.1e-09:393:62//AL010151

R-NT2RP2006100//HS_2020_A2_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2020 Col=4 Row=0, genomic survey sequence.//8.3e-53:304:92//AQ228761

R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) m

RNA, complete cds.//1.5e-16:199:79//M85300
R-NT2RP2006141
R-NT2RP2006166//Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete
sequence.//8.2e-48:329:76//AC002045
R-NT2RP2006184//RPCI11-6016.TP RPCI-11 Homo sapiens genomic clone RPCI-1
1-6016, genomic survey sequence.//0.52:273:61//B49539
R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//1.
9e-108:553:95//AB014554
R-NT2RP2006196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from contig 3-57, complete sequence.//4.2e-05:420:59//AL008981
R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKIN
G DRAFT SEQUENCE, 66 unordered pieces.//2.1e-100:409:96//AC006057
R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//3.8e-93:532:90//X9648
4
R-NT2RP2006237//P.falciparum PK1 gene.//2.9e-08:481:59//X83707
R-NT2RP2006238//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete
sequence.//3.5e-79:405:89//U91318
R-NT2RP2006258//Human PAC clone DJ0899B21 from 7p15-p21, complete sequen
ce.//2.2e-08:283:63//AC004008
R-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK./
/6.2e-13:234:68//X97630
R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.0e-108
:542:97//AF035262
R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J1
6, genomic survey sequence.//1.2e-27:215:65//B17768
R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds.//1.7e-48:29
8:90//U72761
R-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 702J19, WORKING DRAFT SEQUENCE.//2.8e-104:524:96//AL033531

R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.9e-33:298:78//AC004893

R-NT2RP2006334

R-NT2RP2006365//RPC111-72I15.TK RPC111 Homo sapiens genomic clone R-72I15, genomic survey sequence.//2.6e-35:217:92//AQ267043

R-NT2RP2006393//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//8.0e-40:317:81//AC004046

R-NT2RP2006436//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//3.2e-42:184:86//AL022345

R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence.//0.00021:188:68//AF010568

R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence.//0.30:265:60//AE001423

R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence.//2.5e-104:532:96//AF052098

R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//6.6e-108:524:97//AJ006266

R-NT2RP2006467//Sequence 50 from patent US 5691147.//8.3e-22:235:74//I76222

R-NT2RP2006472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE.//5.4e-12:407:62//AL034386

R-NT2RP2006534//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.44:111:65//M25216

R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//0.19:392:58//AE001370

R-NT2RP2006565//Sus scrofa SCAMP1 gene, exon 9.//1.5e-13:292:68//AJ223742

R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence

ence.//0.0024:409:58//AC004660

R-nnnnnnnnnnnnn//Human BRCA2 region, mRNA sequence CG005.//3.3e-16:334:64
//U50532

R-NT2RP2006598//Mus musculus retinoid X receptor interacting protein (RI
P110) mRNA, partial cds.//1.6e-19:448:64//U22015

R-NT2RP3000002//Human DNA sequence from cosmid N104C7 on chromosome 22,
complete sequence.//4.4e-14:501:63//Z82246

R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (J
M21).//5.9e-115:560:97//AJ011972

R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20
unordered pieces.//3.9e-57:402:83//AC005995

R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138_P_22, complet
e sequence.//1.0:158:66//AC005697

R-NT2RP3000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 451B21, WORKING DRAFT SEQUENCE.//2.7e-32:411:69//AL033522

R-NT2RP3000055//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1000N6, WORKING DRAFT SEQUENCE.//7.9e-17:309:69//AL034378

R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds
.//2.9e-07:516:60//D88192

R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence.//1.7e-2
7:186:90//AC005630

R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-conta
ining subunit mRNA, nuclear gene encoding chloroplast protein, complete
cds.//0.0051:289:59//U23155

R-NT2RP3000109//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey s
equence.//2.5e-62:304:100//AQ137776

R-NT2RP3000134//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from MAL1P3, WORKING DRAFT SEQUENCE.//0.027:414:57//AL031746

R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//3.8e-115:578:96//AB011164

R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//1.3e-67:354:95//AC005746

R-NT2RP3000186

R-NT2RP3000197//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat*.//2.5e-31:295:78//Z82899

R-NT2RP3000207//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence.//0.016:305:61//AC004514

R-NT2RP3000220//RPCI11-6307.TJ RPCI11 Homo sapiens genomic clone R-6307, genomic survey sequence.//0.25:118:66//AQ201832

R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195.//3.2e-11:440:59//X15063

R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pD1.//0.81:114:64//U19530

R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1-27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSS and a CA repeat polymorphism, complete sequence.//4.8e-73:362:86//AL023279

R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192_H_23, complete sequence.//0.025:131:66//AC005726

R-NT2RP3000252

R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=16 Row=L, genomic survey sequence.//0.67:119:66//B34879

R-NT2RP3000267

R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.//1.2e-23:424:69//D29766

R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence.//0.55:4

14:59//AL008970

R-NT2RP3000320//HS_3056_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=5 Row=E, genomic survey sequence.//4.1e-32:214:89//AQ134064

R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//1.5e-22:265:75//U78090

R-NT2RP3000333//Plasmodium falciparum MAL3P6, complete sequence.//0.68:460:57//Z98551

R-NT2RP3000341//H.sapiens mRNA for TIM17 preprotein translocase.//1.4e-19:137:90//X97544

R-NT2RP3000348//CITBI-E1-2513C11.TF CITBI-E1 Homo sapiens genomic clone 2513C11, genomic survey sequence.//0.0014:118:72//AQ278177

R-NT2RP3000350

R-NT2RP3000359//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.8e-55:320:75//AC006039

R-NT2RP3000361//Homo sapiens mRNA for KIAA0552 protein, complete cds.//0.18:275:61//AB011124

R-NT2RP3000366//CIT-HSP-2317H13.TF CIT-HSP Homo sapiens genomic clone 2317H13, genomic survey sequence.//6.7e-42:214:100//AQ041634

R-NT2RP3000397//HS-1012-B1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 787 Col=1 Row=L, genomic survey sequence.//0.015:184:63//B31814

R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.3e-109:529:98//AF071185

R-NT2RP3000418//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510B21, WORKING DRAFT SEQUENCE.//6.2e-15:445:65//AL031885

R-NT2RP3000433

R-NT2RP3000439

R-NT2RP3000441

R-NT2RP3000449//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1018D12, WORKING DRAFT SEQUENCE.//1.6e-43:300:76//AL031650
R-NT2RP3000451//3' untranslated region of human mRNA for a K+ channel pr
otein.//0.71:101:66//E13519
R-NT2RP3000456//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A
5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing idurona
te 2-sulfatase gene and pseudogene, complete sequence.//5.2e-16:376:65//
AF011889
R-NT2RP3000484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 120G22, WORKING DRAFT SEQUENCE.//0.61:326:58//AL031847
R-NT2RP3000487//Sequence 32 from patent US 5476781.//8.6e-08:409:61//I16
692
R-NT2RP3000512//RPCI11-60F15.TK RPCI11 Homo sapiens genomic clone R-60F1
5, genomic survey sequence.//2.2e-68:379:93//AQ201516
R-NT2RP3000526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 377F16, WORKING DRAFT SEQUENCE.//4.1e-07:224:65//Z93783
R-NT2RP3000527//HS_3228_A1_H07_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3228 Col=13 Row=0, genomic survey
sequence.//4.5e-30:184:93//AQ209131
R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24,
genomic survey sequence.//0.67:88:68//AQ248538
R-NT2RP3000542//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 126B4, WORKING DRAFT SEQUENCE.//2.0e-24:145:82//AL022316
R-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete seq
uence.//6.1e-107:548:95//AC006012
R-NT2RP3000562//HS_2041_B1_E08_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic survey
sequence.//9.6e-55:279:98//AQ230207
R-NT2RP3000578//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***

from contig 3-105, complete sequence.//0.00060:356:58//AL010212

R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-29:282:67//AC004666

R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//7.4e-44:245:78//AC002377

R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.66:341:59//AC004077

R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.022:491:56//AC005505

R-nnnnnnnnnnnnn//HS_3025_A1_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.//2.6e-21:161:88//AQ101452

R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence.//1.3e-09:543:58//AL034560

R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//5.6e-115:554:98//AC006128

R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces.//0.15:233:63//AC005414

R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence.//1.0:166:66//B64262

R-NT2RP3000628//Human BAC clone GS188P18, complete sequence.//5.3e-56:384:83//AC000115

R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds.//4.0e-61:438:85//U73379

R-NT2RP3000644//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTG, and RAD23A genes, genomic sequence.//1.0e-43:408:77//AD000092

R-NT2RP3000661//F.rubripes GSS sequence, clone 148D22bB9, genomic survey

sequence.//2.7e-17:234:69//AL005927

R-NT2RP3000665//Human chromosome 11 46b2 cosmid, complete sequence.//2.1e-42:526:72//U73645

R-NT2RP3000685//HS_3007_A2_F02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=4 Row=K, genomic survey sequence.//1.6e-101:506:97//AQ118425

R-NT2RP3000690//Plasmodium falciparum MAL3P6, complete sequence.//1.3e-13:411:61//Z98551

R-NT2RP3000736

R-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//0.0071:231:65//U16655

R-NT2RP3000753//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6 . Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.88:366:56//AL021368

R-NT2RP3000759//HS_2055_A2_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=18 Row=G, genomic survey sequence.//0.45:251:60//AQ234828

R-NT2RP3000815//Homo sapiens chromosome 17, clone hRPK.209_J_20, complete sequence.//2.0e-20:293:72//AC005822

R-NT2RP3000825//Plasmodium falciparum MAL3P6, complete sequence.//0.0044:325:62//Z98551

R-NT2RP3000826//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1177I5, WORKING DRAFT SEQUENCE.//5.3e-25:375:72//AL022315

R-NT2RP3000836//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//1.3e-19:181:81//AL022344

R-NT2RP3000841//Homo sapiens, clone hRPK.1_A_1, complete sequence.//0.20

:226:61//AC006196

R-NT2RP3000845//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//6.8e-91:512:92//AC005781

R-NT2RP3000847//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//7.9e-38:179:86//U14572

R-NT2RP3000850//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//4.4e-48:505:76//AC005014

R-NT2RP3000852//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-82:311:98//AL031297

R-NT2RP3000859

R-NT2RP3000865//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//1.2e-15:482:63//AL022153

R-NT2RP3000868//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00045:260:59//AB003097

R-NT2RP3000869//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//0.0058:172:64//AL031731

R-NT2RP3000875//H.sapiens /Hepatitis B virus fusion mRNA for mevalonate kinase.//1.4e-99:531:93//X75311

R-NT2RP3000901

R-NT2RP3000904//Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.//0.32:261:57//AC000348

R-NT2RP3000917//Plasmodium falciparum MAL3P7, complete sequence.//0.00092:456:58//AL034559

R-NT2RP3000919

R-NT2RP3000968//H.sapiens mRNA for ribosomal protein S15a.//4.5e-24:375:71//X84407

R-NT2RP3000980//Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence.//0.36:186:62//AC006079

R-NT2RP3000994//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 geno

mic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC005140

R-NT2RP3001004//*Saccharomyces cerevisiae* VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence.//1.1e-07:330:64//U32857

R-NT2RP3001007//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 4-82, complete sequence.//0.045:286:61//AL010255

R-NT2RP3001055//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.3e-56:348:91//Z95125

R-NT2RP3001057//*H.sapiens* HZF4 mRNA for zinc finger protein.//8.2e-84:531:86//X78927

R-NT2RP3001081//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//1.1e-08:537:60//AL031746

R-NT2RP3001084

R-NT2RP3001096

R-NT2RP3001107

R-nnnnnnnnnnnn//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//7.4e-62:272:73//AC005316

R-NT2RP3001111

R-NT2RP3001113

R-NT2RP3001115//*Homo sapiens* PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-112:550:97//AC005189

R-NT2RP3001116//CIT-HSP-2282K23.TR CIT-HSP *Homo sapiens* genomic clone 2282K23, genomic survey sequence.//0.00013:160:69//AQ002011

R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequ

ence.//5.9e-99:497:96//AL031864

R-NT2RP3001120

R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence.//0.035:266:56//AL034559

R-NT2RP3001133

R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//8.1e-114:549:97//AB018305

R-NT2RP3001147//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.69:198:63//AC004448

R-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.4e-108:542:97//AL034379

R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//2.9e-116:563:98//AJ006266

R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.44:227:62//AC004688

R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence.//0.0023:381:61//AE000785

R-NT2RP3001216//RPCI11-18C15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-18C15, genomic survey sequence.//7.0e-29:167:97//B88077

R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.020:211:63//AC005827

R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6 q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.7e-08:390:62//AL021326

R-NT2RP3001236//RPCI11-25C17.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25C17, genomic survey sequence.//9.5e-41:217:88//AQ014003

R-NT2RP3001239//Human microtubule-associated protein 1B (MAP1B) gene, complete cds.//2.9e-21:438:63//L06237

R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chromosome 1q24-q25. Contains EST, GSS.//0.00026:439:59//AL021398

R-NT2RP3001253//HS_3002_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=24 Row=0, genomic survey sequence.//0.98:190:63//AQ251982

R-NT2RP3001260

R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.012:509:57//AC004936

R-NT2RP3001272//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//2.2e-22:134:87//AC005589

R-NT2RP3001274//Sequence 11 from Patent W09517522.//0.0058:133:66//A45341

R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//4.4e-55:558:76//Z96811

R-NT2RP3001307//HS_2058_A1_C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=11 Row=E, genomic survey sequence.//7.2e-33:260:86//AQ305868

R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.27:210:65//AC004848

R-NT2RP3001325

R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial).//1.0:184:64//M86367

R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds.//1.2e-112:566:96//AB007920

R-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//3.2e-86:450:95//AF083105

R-NT2RP3001355

R-NT2RP3001374//HS_2184_A2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2184 Col=8 Row=M, genomic survey s

equence.//3.7e-10:101:84//AQ024647

R-NT2RP3001383//Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence.//7.4e-07:279:63//AE001397

R-NT2RP3001384//Homo sapiens chromosome 19, cosmid R33907, complete sequence.//4.4e-75:382:97//AC005785

R-NT2RP3001392//HS_3078_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=10 Row=H, genomic survey sequence.//1.0:164:64//AQ140587

R-NT2RP3001396//RPCI11-63N18.TJ RPCI11 Homo sapiens genomic clone R-63N18, genomic survey sequence.//0.14:242:61//AQ238544

R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.8e-10:193:72//U49046

R-NT2RP3001399

R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequence.//0.0011:392:60//Z68160

R-NT2RP3001420//Human BAC clone GS165I04 from 7q21, complete sequence.//3.7e-29:412:74//AC002379

R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence.//1.1e-104:550:94//AF052158

R-NT2RP3001427//Caenorhabditis elegans cosmid K11D5.//0.39:174:64//U53152

R-nnnnnnnnnnnnn//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//1.4e-94:533:91//U69668

R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence.//2.5e-12:415:61//AL009029

R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.6e-36:358:77//AC004903

R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence.//1.5e-100:499:97

//AF070630

R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-47:295:86//AC004906

R-NT2RP3001457

R-NT2RP3001459

R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b gRNA-mRNA chimera, clone:24.//0.33:150:66//D13030

R-NT2RP3001490//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, complete sequence.//2.3e-08:483:60//AL010208

R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//4.4e-60:338:93//U13395

R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.1e-110:549:97//AF064801

R-NT2RP3001527//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//5.3e-32:310:78//AL034549

R-NT2RP3001529//Human Chromosome X, complete sequence.//5.5e-67:280:93//AC002420

R-NT2RP3001538

R-NT2RP3001554//Human microtubule-associated protein 1a (MAP1A) mRNA, complete cds.//7.8e-16:391:62//U38292

R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00026:456:58//AC004688

R-NT2RP3001587//Homo sapiens HRIHFB2115 mRNA, partial cds.//5.6e-08:86:88//AB015337

R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//0.066:360:60//AC005410

R-NT2RP3001607//CIT-HSP-2010M8.TR CIT-HSP Homo sapiens genomic clone 2010M8, genomic survey sequence.//0.041:194:67//B53490

R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//0.69:151:64//Z83821

R-NT2RP3001621//Human DNA sequence from clone 24018 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.4e-46:354:83//AL021808

R-NT2RP3001629//H.sapiens simple DNA sequence region clone wgl10.//0.99:137:63//X76572

R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds.//8.5e-108:541:96//AF099149

R-NT2RP3001642

R-NT2RP3001646//HS_3218_A2_A01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=2 Row=A, genomic survey sequence.//2.6e-32:215:91//AQ303003

R-NT2RP3001671//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-88, complete sequence.//0.018:262:61//AL010157

R-NT2RP3001672

R-NT2RP3001676//Homo sapiens cosmid Q95D4, chromosome 21 5' of IFNAR2.//2.1e-48:413:77//AF039905

R-NT2RP3001678//RPCI11-50C17.TK RPCI11 Homo sapiens genomic clone R-50C17, genomic survey sequence.//0.15:232:62//AQ116359

R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//7.8e-104:549:95//AB020860

R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//6.6e-41:291:86//AC006019

R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//3.1e-07:433:59//AE001415

R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence.//6.0e-06:237:64//AF053523

R-NT2RP3001712//CITBI-E1-2516N9.TF CITBI-E1 Homo sapiens genomic clone 2516N9, genomic survey sequence.//1.5e-95:456:99//AQ279562

R-NT2RP3001716//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0012:346:58//AC004617

R-NT2RP3001724//Human HepG2 3' region MboI cDNA, clone hmd6a06m3.//1.3e-27:163:95//D17273

R-NT2RP3001730//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.//7.6e-43:409:76//Z98200

R-NT2RP3001739

R-NT2RP3001752//Human clone 23774 mRNA sequence.//1.9e-08:104:84//U79279

R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey sequence.//8.8e-06:102:78//AQ113378

R-NT2RP3001764

R-NT2RP3001777//Human mRNA for heparan sulfate proteoglycan (glypican).//0.99:166:66//X54232

R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//1.3e-111:549:97//AB007928

R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.6e-32:266:83//U13262

R-NT2RP3001799//H.sapiens mRNA for OX40 homologue.//8.5e-44:374:79//X75962

R-NT2RP3001819

R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7.//0.0042:231:63//U40410

R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (

HSP86), 01 (o1), 03 (o3), 02 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//1.0:404:59//AF030694

R-NT2RP3001855

R-NT2RP3001896//CIT978SK-A-636F10.TV CIT978SK Homo sapiens genomic clone A-636F10, genomic survey sequence.//0.0012:68:82//AQ116409

R-NT2RP3001898//Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.//0.37:266:65//AC005950

R-NT2RP3001915//Human BAC clone RG367017 from 7p15-p21, complete sequence.//0.018:144:66//AC002486

R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds.//2.4e-10:77:100//M77142

R-NT2RP3001929

R-NT2RP3001931//Homo sapiens full length insert cDNA clone YU73B11.//1.0e-110:562:96//AF087969

R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome Xq13.1-Xq13.3.//0.38:386:56//Z95328

R-NT2RP3001943//Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.//0.87:298:61//AC004500

R-NT2RP3001944//Bos taurus clone CSSM056 satellite DNA sequence.//0.0095:76:78//U03836

R-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//7.0e-109:552:96//AC005844

R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.15:111:68//Z81029

R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987

R-NT2RP3002004//H.sapiens mRNA for FAST kinase.//5.1e-41:335:82//X86779

R-NT2RP3002007

R-NT2RP3002014//Human DNA sequence from clone 228A9 on chromosome 22q12.3-13.32 Contains 85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A2, EST, GSS, CpG island, complete sequence.//6.6e-41:297:86//AL022322

R-NT2RP3002033

R-NT2RP3002045//Drosophila melanogaster fat protein (fat) gene, complete cds.//0.77:320:60//M80537

R-NT2RP3002054//Caenorhabditis elegans cosmid Y69H2, complete sequence.//0.82:362:57//Z98877

R-NT2RP3002056//F.rubripes GSS sequence, clone 020E22bF7, genomic survey sequence.//0.010:185:63//Z87006

R-NT2RP3002057

R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-17:164:81//AC004002

R-nnnnnnnnnnnnnnn

R-NT2RP3002081//HS_3082_A1_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=17 Row=M, genomic survey sequence.//4.2e-25:344:73//AQ122260

R-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//2.6e-23:212:80//AC006210

R-NT2RP3002102//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//0.43:168:64//AC004746

R-NT2RP3002108//CIT-HSP-2346P16.TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey sequence.//3.5e-08:110:78//AQ059071

R-NT2RP3002146//Streptococcus gordonii competence factor (comC) and histidine protein kinase (comD) genes, complete cds, and response regulator (comE) gene, partial cds.//0.11:534:55//U80077

R-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE.//4.1e-108:551:96//AL031710

R-NT2RP3002151//Mus musculus mRNA for Guanine Nucleotide Regulatory Protein, complete cds.//6.8e-62:347:80//AB003503

R-NT2RP3002163//Anolis pulchellus vitellogenin mRNA, partial cds.//0.77:281:63//U46857

R-NT2RP3002165

R-NT2RP3002166//D.sargus satellite DNA (clone PSE3).//0.81:124:62//Z4871
1

R-NT2RP3002173

R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library C
Homo sapiens genomic clone Plate=CT 824 Col=2 Row=K, genomic survey sequence.//1.3e-35:305:81//B36980

R-NT2RP3002244//Caenorhabditis elegans cosmid R11E3.//0.0024:393:61//AF1
00669

R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 22q12-q
ter contains ESTs.//0.30:217:63//Z82189

R-NT2RP3002255

R-NT2RP3002273//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//0.84:463:57//AF070717

R-NT2RP3002276//HS_2260_A1_MF_E07 CIT Approved Human Genomic Sperm Library D
Homo sapiens genomic clone Plate=2260 Col=13 Row=I, genomic survey sequence.//0.0017:198:63//AQ292491

R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17.//7.4e-93:510:93//X13546

R-NT2RP3002304//Human BAC clone GS188P18, complete sequence.//6.3e-09:47
7:59//AC000115

R-NT2RP3002330//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic
sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.087:388:58//AC0
04688

R-NT2RP3002343

R-NT2RP3002351//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.20:489:56//AC004617

R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene.//2.4e-104:516:94//Y15164

R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//4.7e-102:524:95//AB014578

R-NT2RP3002484

R-NT2RP3002501//Human DNA sequence from PAC 92M18, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 25, 26 and 27 ESTs and STS.//5.2e-17:232:75//Z73359

R-NT2RP3002512

R-NT2RP3002529//CIT-HSP-2340H2.TR CIT-HSP Homo sapiens genomic clone 234 OH2, genomic survey sequence.//0.81:266:58//AQ057387

R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//3.3e-82:438:94//AB018272

R-NT2RP3002549//Medicago truncatula ENBP1 gene, exons 1 to 12.//0.95:381:56//AJ002479

R-NT2RP3002566//HS_2036_A1_D08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=15 Row=G, genomic survey sequence.//0.18:162:64//AQ230627

R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-15:213:73//AC004956

R-NT2RP3002590//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MXK3, complete sequence.//0.00010:431:59//AB019236

R-NT2RP3002602//Mus musculus stannin gene, complete cds.//1.6e-20:339:70//AF030522

R-NT2RP3002603

R-NT2RP3002631//Homo sapiens chromosome 21 PAC RPCIP704A9190Q2.//1.0:241:59//AJ006997

R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) m
RNA, complete cds.//6.8e-24:331:76//M85300

R-NT2RP3002660//H.sapiens partial gene for progesterone receptor and Alu
element DNA.//9.8e-43:273:82//Z49816

R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial
gene encoding ribosomal RNA, partial sequence.//0.60:300:59//U82072

R-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.2e-20:399:66//AL0
23704

R-NT2RP3002682//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6,
genomic survey sequence.//4.7e-09:122:77//AQ202481

R-NT2RP3002687//P.falciparum complete gene map of plastid-like DNA (IR-B
).//1.1e-07:494:59//X95276

R-NT2RP3002688//Human 7SL RNA sequence.//2.7e-32:290:79//X01037

R-NT2RP3002701

R-NT2RP3002713//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 167A19, WORKING DRAFT SEQUENCE.//0.95:334:59//AL031427

R-NT2RP3002763//***ALU WARNING: Human Alu-J subfamily consensus sequence
.//3.9e-40:288:85//U14567

R-NT2RP3002770//R.prowazekii genomic DNA fragment (clone A615F).//0.21:1
74:63//Z82710

R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete seq
uence.//0.78:354:59//AC004822

R-NT2RP3002799//Homo sapiens X-linked anhidrotic ectodermal dysplasia p
rotein gene (EDA), exon 2 and flanking repeat regions.//1.1e-20:161:77//
AF003528

R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2.//0.28:441:56//AF022
972

R-NT2RP3002818//HS_3053_A2_A08_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3053 Col=16 Row=A, genomic survey

sequence.//0.19:220:60//AQ135025

R-NT2RP3002861//P.falciparum complete gene map of plastid-like DNA (IR-B).//9.3e-05:414:60//X95276

R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//0.14:165:64//AC005256

R-NT2RP3002876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.6e-59:311:96//AL034380

R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.6e-24:422:63//AC003035

R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//4.7e-109:570:95//AB018314

R-NT2RP3002911//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//3.1e-16:471:64//AC005014

R-NT2RP3002948//, complete sequence.//4.5e-94:516:93//AC005500

R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.4e-111:566:96//AC005754

R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//0.19:424:58//AE001391

R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.1e-89:562:88//D30666

R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence.//1.0:122:67//AF067482

R-NT2RP3002978//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//4.8e-05:249:63//AL031733

R-NT2RP3002988//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.0097:246:67//Z97195

R-NT2RP3003008//Mus musculus major histocompatibility locus class III re

gions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.9e-24:188:78//AF109905

R-NT2RP3003032//Arabidopsis thaliana (clone DW1) DNA retrotransposon Tal1-1 integration site.//5.3e-07:376:63//L47211

R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence.//1.4e-13:323:66//AC005669

R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-10).//3.8e-42:265:91//Y16708

R-NT2RP3003068//HS_3214_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=18 Row=N, genomic survey sequence.//0.025:207:64//AQ181894

R-NT2RP3003071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-NT2RP3003078//T26A1TF TAMU Arabidopsis thaliana genomic clone T26A1, genomic survey sequence.//0.95:219:63//B27013

R-NT2RP3003101//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-05:285:62//AC004153

R-NT2RP3003121//Homo sapiens full length insert cDNA clone ZD62D10.//2.1e-47:242:98//AF086348

R-NT2RP3003133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.4e-21:199:75//AL031985

R-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.1e-14:287:68//D12646

R-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//1.5e-13:122:80//U17995

R-NT2RP3003150

R-NT2RP3003157//Homo sapiens 12q15 BAC GSHB-410F4 (Genome Systems Human

Bac Library) complete sequence.//5.5e-42:289:74//AC005294
R-NT2RP3003185//HS_2058_A1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=5 Row=0, genomic survey sequence.//0.025:52:94//AQ231298
R-NT2RP3003193//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//4.8e-40:349:79//AC005701
R-NT2RP3003197//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 364I1, WORKING DRAFT SEQUENCE.//5.2e-10:180:71//AL031319
R-NT2RP3003203//Mus musculus IFN alpha-treated embryonic fibroblast mRNA .//1.8e-11:148:77//U51904
R-NT2RP3003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 892F13, WORKING DRAFT SEQUENCE.//6.6e-41:282:86//AL009183
R-NT2RP3003212//Homo sapiens full length insert cDNA clone ZB91B11.//1.7e-68:363:95//AF086173
R-NT2RP3003230//Caenorhabditis elegans cosmid T12B5.//0.0018:279:64//AF100307
R-NT2RP3003242//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.0:346:57//AC005272
R-NT2RP3003251//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//2.5e-10:436:62//AC003083
R-NT2RP3003264//CIT-HSP-2296M7.TR CIT-HSP Homo sapiens genomic clone 2296M7, genomic survey sequence.//5.8e-05:308:61//AQ005862
R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3b11m5.//9.4e-47:302:89//D17022
R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//7.4e-101:550:93//L36983
R-NT2RP3003290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//3.0e-22:228:78//AL031662
R-NT2RP3003301

R-NT2RP3003302//CIT-HSP-2319H19.TF CIT-HSP Homo sapiens genomic clone 2319H19, genomic survey sequence.//1.5e-69:367:95//AQ034950

R-NT2RP3003311//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//5.1e-08:398:64//AC005505

R-NT2RP3003313//Caenorhabditis elegans cosmid F39B1, complete sequence.//0.00022:436:58//Z69660

R-NT2RP3003327//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-237H1 complete genomic sequence, complete sequence.//1.5e-16:334:70//AC002287

R-NT2RP3003330//Homo sapiens full length insert cDNA YI24C02.//4.4e-96:458:99//AF075015

R-NT2RP3003344//HS_3235_B2_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=18 Row=P, genomic survey sequence.//4.1e-18:197:80//AQ303203

R-NT2RP3003346

R-NT2RP3003353//CITBI-E1-2523B18.TR CITBI-E1 Homo sapiens genomic clone 2523B18, genomic survey sequence.//8.3e-06:130:73//AQ278834

R-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.9e-97:481:94//AC005519

R-NT2RP3003384//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-10:226:71//AC004820

R-NT2RP3003385

R-NT2RP3003403//Human DNA sequence from clone 227L5 on chromosome Xp11.2-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, C K18) pseudogene and an STS, complete sequence.//2.8e-40:496:72//AL031585

R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA.//1.5e-20:375:68//L23204

R-NT2RP3003411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 438L4, WORKING DRAFT SEQUENCE.//1.0:180:61//Z97635

R-NT2RP3003427//RPCI11-45J23.TJ RPCI11 Homo sapiens genomic clone R-45J23, genomic survey sequence.//0.82:162:69//AQ195566

R-NT2RP3003433//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//1.1e-10:379:61//AC006031

R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//1.1e-95:479:96//AF004828

R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.3e-100:527:93//AB018268

R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-08:495:59//AE001398

R-NT2RP3003500//W.suaveolens mitochondrial ATP9 gene.//0.0074:514:59//X77238

R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA.//1.3e-31:217:88//U00952

R-NT2RP3003552

R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, complete cds.//0.98:321:61//AF057019

R-NT2RP3003564

R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22q12.1 contains STS.//0.0015:507:59//AL008638

R-NT2RP3003576//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//1.2e-39:359:79//AC003007

R-NT2RP3003589//Plasmodium falciparum MAL3P8, complete sequence.//0.014:539:58//AL034560

R-NT2RP3003625//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//1.8e-44:448:77//AL022238

R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//0.34:257:62//AC005291

R-NT2RP3003659//O.fuscipennis 16S rRNA gene, partial.//0.021:145:65//Z93701

R-NT2RP3003665//HS_3078_B2_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=18 Row=F, genomic survey sequence.//1.3e-75:397:95//AQ140580

R-NT2RP3003672

R-NT2RP3003686

R-NT2RP3003701//Human BAC clone GS310A05 from 7q21-q22, complete sequence.//6.4e-17:464:62//AC002452

R-NT2RP3003716//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE.//0.00072:425:62//AL034410

R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//1.7e-101:492:97//AB018300

R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//3.7e-07:217:66//AC003009

R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//8.1e-26:456:68//Z98052

R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-138g10, genomic survey sequence.//4.9e-09:117:77//B01736

R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds.//2.8e-106:551:95//AF077754

R-NT2RP3003805

R-NT2RP3003809//Homo sapiens full length insert cDNA clone YZ95A01.//3.6e-106:533:97//AF086107

R-NT2RP3003819//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 34606, WORKING DRAFT SEQUENCE.//6.0e-44:288:81//Z84487
R-NT2RP3003825//Mus domesticus interleukin 1 receptor antagonist (IL-1RA
) mRNA.//0.0014:410:58//M64404
R-NT2RP3003828
R-NT2RP3003831//***ALU WARNING: Human Alu-J subfamily consensus sequence
./2.3e-41:289:85//U14567
R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.6e
-108:541:97//AF070611
R-NT2RP3003842//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library
) complete sequence.//1.5e-46:457:74//AC002980
R-NT2RP3003846//Plasmodium falciparum MAL3P3, complete sequence.//3.5e-0
6:356:62//Z98547
R-NT2RP3003870//Homo sapiens full length insert cDNA clone ZD75H11.//8.2
e-09:68:98//AF086402
R-NT2RP3003876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1018D12, WORKING DRAFT SEQUENCE.//0.0027:180:66//AL031650
R-NT2RP3003914//Dictyostelium discoideum DNA for transposable element Td
d-3 tandem array.//0.029:234:62//X53439
R-NT2RP3003918
R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, a
nd complete cds.//0.00087:164:67//AF029215
R-NT2RP3003989
R-NT2RP3003992//Sequence 1 from patent US 5591825.//0.56:235:59//I33465
R-NT2RP3004013//HS_3018_A1_G09_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3018 Col=17 Row=M, genomic survey
sequence.//0.00026:421:60//AQ119904
R-NT2RP3004016//Drosophila melanogaster DNA sequence (P1s DS03465 (D149)
and DS08544 (D187)), complete sequence.//4.8e-12:308:62//AC004532
R-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 598F2, WORKING DRAFT SEQUENCE.//0.42:190:64//AL021579
R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//3.6e-21:332:69//AC006130
R-NT2RP3004070//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.0e-05:476:57//AC005308
R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complete sequence.//2.0e-86:486:93//AC005784
R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete sequence.//5.3e-11:230:69//AC002525
R-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-93:551:92//AC005038
R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-104:317:100//AC006064
R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus).//0.73:168:60//U36532
R-NT2RP3004145//Homo sapiens full length insert cDNA clone ZE09H03.//2.3e-89:427:99//AF086542
R-NT2RP3004148//Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence.//0.013:134:70//U78721
R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//3.8e-10:101:87//AC004081
R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence.//1.5e-06:442:57//AC005533
R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6.//1.7e-07:220:69//D29763
R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.

ce.//7.3e-89:504:92//D42052

R-NT2RP3004215//Caenorhabditis elegans cosmid F11A6, complete sequence./
/0.018:353:59//Z81498

R-NT2RP3004242//Plasmodium falciparum chromosome 2, section 52 of 73 of
the complete sequence.//4.5e-06:407:60//AE001415

R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q
25, complete sequence.//2.8e-105:534:97//AC005385

R-NT2RP3004253//RPCI11-78J12.TJ RPCI11 Homo sapiens genomic clone R-78J1
2, genomic survey sequence.//4.0e-64:382:90//AQ281324

R-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//7.0e-60:417:8
4//AF013967

R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete c
ds.//2.7e-43:528:73//AF092536

R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPC.1110_E_20, comple
te sequence.//1.4e-06:435:62//AC004231

R-NT2RP3004341//CITBI-E1-2503F11.TR CITBI-E1 Homo sapiens genomic clone
2503F11, genomic survey sequence.//0.0018:210:65//AQ263365

R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete
sequence.//7.1e-46:340:83//AC005695

R-NT2RP3004349//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 11703, WORKING DRAFT SEQUENCE.//9.4e-29:263:79//AL020995

R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-X
p11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repe
ats.//2.0e-67:422:90//Z95125

R-NT2RP3004399//HS_3046_A1_E02_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3046 Col=3 Row=I, genomic survey s
equence.//0.00014:186:67//AQ137619

R-NT2RP3004424//RPCI11-59I14.TJ RPCI11 Homo sapiens genomic clone R-59I1
4, genomic survey sequence.//7.4e-71:370:95//AQ201461

R-NT2RP3004428//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
 * from clone Y66A7, WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282
 R-NT2RP3004451//Arabidopsis thaliana chromosome II BAC F15K20 genomic se
 quence, complete sequence.//0.0029:396:60//AC005824
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2
 .9e-106:526:98//AB007917
 R-NT2RP3004466
 R-NT2RP3004470//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), co
 mplete sequence.//8.3e-06:229:64//AC005895
 R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomi
 c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC
 005504
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.
 6e-105:521:97//AB007925
 R-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete
 cds.//3.9e-38:322:81//U47024
 R-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence
 .//4.2e-96:527:92//AC003982
 R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25
 unordered pieces.//2.3e-43:342:82//AC006023
 R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:
 68//AC000357
 R-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.8e-28:387:70//Y0826
 0
 R-NT2RP3004507
 R-NT2RP3004527//Homo sapiens chromosome 14, BAC CITB-135H17 containing
 the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518
 R-nnnnnnnnnnnnn//Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:8
 4//L11316

R-NT2RP3004544

R-NT2RP3004566

R-NT2RP3004569//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709

R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083

R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946

R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234

R-NT2RP3004617

R-NT2RP3004618//F2H16TF, IGF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414

R-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679

R-NT2RP4000008//H.sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749

R-NT2RP4000023//CIT-HSP-2372A9.TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388

R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015

R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266

R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b In DGCR Region, complete sequence.//0.56:462:58//AC000074

R-NT2RP4000078//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00021:460:60//AC005506

R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148),
complete sequence.//1.6e-08:518:58//AC004648
R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//3.5e-106:536:
96//AB011538
R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.
1e-110:554:97//AB007952
R-NT2RP4000147
R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:
395:83//L20681
R-NT2RP4000151
R-NT2RP4000159//Caenorhabditis elegans cosmid R02F11.//0.00011:261:63//A
F016439
R-NT2RP4000167//RPC111-59L8.TK RPC111 Homo sapiens genomic clone R-59L8,
genomic survey sequence.//6.2e-26:163:93//AQ200049
R-NT2RP4000185
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.
6e-99:505:96//AB014600
R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300
R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete seq
uence.//1.2e-39:272:88//AC005261
R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete seq
uence.//1.6e-09:457:60//AC004081
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP
).//9.0e-69:354:96//AJ006470
R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0
e-27:344:73//D10727
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence./
/9.7e-78:381:99//AF091092
R-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 23

36N24, genomic survey sequence.//0.26:124:69//AQ043515
R-nnnnnnnnnnnnn//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri HVS, host-squirrel monkey, Genomic, 4 genes, 3720 nt].//0.12:326:61//S76368
R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS and GSSs, complete sequence.//2.2e-111:538:98//AL033384
R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524
R-NT2RP4000323//S.cerevisiae telomeric sequence DNA, clone YLP108CA-2-i.//0.048:107:69//M34311
R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-39:350:79//AC004972
R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281
R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.7e-109:527:98//AF044195
R-NT2RP4000370//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//9.9e-25:348:72//AC005154
R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.//2.2e-69:391:89//U17901
R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//0.066:197:63//AC006080
R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey sequence.//0.10:79:75//B15527
R-NT2RP4000417//Homo sapiens full length insert cDNA clone ZD52B10.//9.6e-96:468:97//AF086313
R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase

2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//1.8e-08:489:59//AL021026

R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505

R-NT2RP4000449//HS_2037_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047

R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271

R-nnnnnnnnnnnnnnn

R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082

R-nnnnnnnnnnnnnnn

R-NT2RP4000500

R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140

R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:77//AC003007

R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence.

nce (GSS), complete sequence.//0.0080:461:59//AL021068
R-NT2RP4000519
R-NT2RP4000524
R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.//0.99:158:66//AC005697
R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e In DGCR Region, complete sequence.//1.0:309:59//AC000078
R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene, complete cds.//0.0031:126:72//AF052695
R-NT2RP4000588//Homo sapiens BAC clone RG208K23 from 7q31, complete sequence.//1.0:186:64//AC004161
R-NT2RP4000614//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-62, complete sequence.//1.4e-06:526:58//AL009013
R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.9e-48:497:75//AC004666
R-NT2RP4000648//CIT-HSP-2300I7.TR CIT-HSP Homo sapiens genomic clone 2300I7, genomic survey sequence.//0.22:110:68//AQ012747
R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene, clone 5' LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds.//0.0065:189:63//U20443
R-NT2RP4000704//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//0.22:334:60//Z83824
R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c In DGCR Region, complete sequence.//2.2e-70:448:88//AC000080
R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sapiens genomic clone 2310K14, genomic survey sequence.//0.00013:289:61//AQ019669
R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.53:254:61//AC004765
R-NT2RP4000781//P.cepacia fusaric acid-resistance genes encoding 5 prote

ins, complete cds.//1.0:392:59//D12503

R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//0.59:378:58//AC003037

R-NT2RP4000833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//3.4e-53:307:85//AL023808

R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//7.0e-50:367:77//AE000660

R-NT2RP4000855

R-NT2RP4000865//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//1.5e-78:479:88//AC003098

R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//4.5e-09:186:69//AJ001616

R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-08:364:60//AC004153

R-nnnnnnnnnnnn//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M88006

R-nnnnnnnnnnnn//H.sapiens ung gene for uracil DNA-glycosylase.//7.6e-09:392:61//X89398

R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//5.8e-45:264:92//U42975

R-nnnnnnnnnnnn//epstein-barr virus simple repeat array (ir3).//0.00012:367:61//J02079

R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MCL19, complete sequence.//1.0:138:68//AB006698

R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//0.45:288:62//Z82197

R-NT2RP4000955//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 633019, WORKING DRAFT SEQUENCE.//1.1e-09:322:62//AL022302
R-NT2RP4000973//Homo sapiens X-linked anhidrotic ectodermal dysplasia p
rotein gene (EDA), exon 2 and flanking repeat regions.//2.3e-06:326:62//
AF003528
R-NT2RP4000975
R-NT2RP4000979//HS_3009_B1_F08_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3009 Col=15 Row=L, genomic survey
sequence.//2.3e-14:117:89//AQ090957
R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotei
n (env) gene, C2-V3 region, isolate HIV194UG011INT.01_di1PD, partial cds
.//0.11:219:62//U44882
R-NT2RP4000989//Sequence 30 from patent US 5552281.//3.5e-25:154:97//I25
669
R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), 01 (o1), 03 (o3), 02 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694
R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003
R-NT2RP4001004//HS_3163_A2_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=0, genomic survey sequence.//2.8e-38:241:90//AQ168515
R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//7.1e-55:372:73//AC006023
R-NT2RP4001010//Homo sapiens full length insert cDNA clone ZD38E12.//3.3e-09:153:74//AF086247
R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20086
R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192),

complete sequence.//9.9e-84:435:96//AC005216

R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94
//AB007859

R-NT2RP4001064//H.sapiens NOS2 gene, exon 15.//0.71:183:61//X85771

R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete c
ds.//1.9e-114:569:97//U48213

R-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase,
partial.//2.4e-118:574:98//AJ010953

R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of
the complete sequence.//0.013:430:58//AE001429

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.
8e-119:548:95//AB011164

R-NT2RP4001095//Homo sapiens cosmids IM0525, LC1233, Qc3C1, LB1439, Qc12
C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626

R-NT2RP4001100//Human DNA sequence from cosmid U85A3, between markers DX
S366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pse
udogenes, STS.//8.7e-41:389:78//Z78021

R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.
8e-12:292:68//M96629

R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.
//0.97:129:66//Z68298

R-NT2RP4001126//HS_3146_A1_B05_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey s
equence.//0.013:268:63//AQ141093

R-NT2RP4001138

R-NT2RP4001143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 64K7, WORKING DRAFT SEQUENCE.//1.8e-31:380:68//AL031668

R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 u
nordered pieces.//1.2e-83:325:92//AC005095

R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067

R-NT2RP4001150//AK011 Genomic DNA Hordeum vulgare genomic clone tel44a similar to barley TAS, genomic survey sequence.//0.91:132:63//AQ248412

R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468

R-NT2RP4001174//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//1.7e-33:289:82//AC002996

R-nnnnnnnnnnnnn//P.falciparum mRNA for AARP2 protein.//0.93:187:64//Y08924

R-NT2RP4001207

R-NT2RP4001210//CIT-HSP-2042D13.TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772

R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66//M99593

R-NT2RP4001219//HS_2190_A1_A06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence.//2.4e-06:288:61//AQ216635

R-NT2RP4001228//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.024:357:58//AL031745

R-NT2RP4001235//HS_3047_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=I, genomic survey sequence.//0.0033:301:63//AQ126918

R-NT2RP4001256//HS_3007_A2_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389

R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//0.0013:486:59//AE001426

R-NT2RP4001274//RPCI11-24021.TKBF RPCI-11 Homo sapiens genomic clone RPC I-11-24021, genomic survey sequence.//3.9e-25:142:99//AQ013887
R-nnnnnnnnnnnnn//Homo sapiens full length insert cDNA clone ZD55D10.//1.2e-10:90:92//AF086334
R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//7.7e-23:466:66//AF009326
R-NT2RP4001315//CIT-HSP-2312C6.TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey sequence.//0.98:305:62//AQ018036
R-NT2RP4001339
R-NT2RP4001345
R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00082:260:59//AB003097
R-NT2RP4001353//RPCI11-55N17.TJ RPCI11 Homo sapiens genomic clone R-55N17, genomic survey sequence.//0.74:106:66//AQ081821
R-NT2RP4001372
R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//1.5e-09:473:60//AC006080
R-NT2RP4001375
R-NT2RP4001379//CIT-HSP-2335A10.TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey sequence.//9.4e-41:441:75//AQ040083
R-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.4e-22:276:73//AC004691
R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.49:254:61//AC005140
R-NT2RP4001414
R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7.//6.6e-66:357:90//L14272
R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic

sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.11:307:59//AC005308

R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-58d2, genomic survey sequence.//0.0039:112:71//B05220

R-NT2RP4001474

R-NT2RP4001483

R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.//1.2e-07:339:61//L34027

R-NT2RP4001502//HS_2187_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2187 Col=19 Row=F, genomic survey sequence.//1.3e-20:183:81//AQ214108

R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.15:333:62//AC005916

R-NT2RP4001524//Genomic sequence from Human 13, complete sequence.//0.96:159:65//AC001226

R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//9.5e-34:337:80//U20086

R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00027:336:63//AC004710

R-nnnnnnnnnnnn//Arabidopsis thaliana BAC T12H20.//1.5e-11:517:60//AF080119

R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs.//0.0069:305:62//Z82212

R-NT2RP4001567//RPCI11-61A2.TJ RPCI11 Homo sapiens genomic clone R-61A2, genomic survey sequence.//0.0072:180:60//AQ200771

R-NT2RP4001568

R-NT2RP4001571//Trypanoplasma borreli kinetoplast ribosomal protein S12

(RPS12), putative cryptogene (GR11), 12S ribosomal RNA, and apocytochrome b (CYb) genes, primary transcripts, and cytochrome c oxidase subunit I II (COIII) gene, complete cds.//1.6e-09:555:58//U14181

R-NT2RP4001574//HS_2247_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=D, genomic survey sequence.//1.1e-41:254:90//AQ182345

R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21 .2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSS, and GSSs, complete sequence.//1.1e-118:567:98//AL031228

R-NT2RP4001592//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//2.5e-09:370:61//AL031650

R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//0.99:73:75//AC002364

R-NT2RP4001614

R-NT2RP4001634//Homo sapiens full length insert cDNA clone YU73B11.//5.8e-101:526:94//AF087969

R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:97//AF007151

R-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092

R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENC

E, 8 unordered pieces.//2.2e-109:515:99//AC000384
R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.
19:504:58//AC000397
R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete seque
nce.//4.5e-115:583:96//U96629
R-NT2RP4001725//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE,
2 unordered pieces.//0.98:301:60//AC000380
R-nnnnnnnnnnnnn//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U2
8735
R-NT2RP4001739//RPCI11-74E7.TJ RPCI11 Homo sapiens genomic clone R-74E7,
genomic survey sequence.//1.1e-08:141:65//AQ268408
R-NT2RP4001753//H.sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:5
52:96//X78926
R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:7
2//L11316
R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 u
nordered pieces.//1.7e-99:484:98//AC005020
R-NT2RP4001803//HS_3087_B2_B05_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey
sequence.//2.7e-96:471:97//AQ121405
R-NT2RP4001822
R-NT2RP4001823
R-NT2RP4001828//Human DNA sequence from PAC 179I15, BRCA2 gene region ch
romosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83/
/Z92540
R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of t
he complete sequence.//2.5e-06:418:60//AE001372
R-NT2RP4001849//P.falciparum serine rich protein (SERP I) gene.//0.64:13
5:67//J03983

R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548

R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014

R-NT2RP4001896

R-NT2RP4001901

R-NT2RP4001927//Borrelia burgdorferi (section 32 of 70) of the complete genome.//1.0:242:60//AE001146

R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//M55523

R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157

R-NT2RP4001950//RPCI11-69C18.TJ RPCI11 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641

R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome X p22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z93023

R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148

R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3' UTR region.//1.0e-46:242:98//U25276

R-NT2RP4002018//RPCI11-76I23.TV RPCI11 Homo sapiens genomic clone R-76I23, genomic survey sequence.//7.9e-89:438:97//AQ268536

R-NT2RP4002047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297

R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353

R-NT2RP4002058//RPCI11-6901.TJ RPCI11 Homo sapiens genomic clone R-6901,

genomic survey sequence.//0.23:163:64//AQ268418

R-NT2RP4002071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386

R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.085:350:61//AL033375

R-NT2RP4002078//RPCI11-79I16.TV RPCI11 Homo sapiens genomic clone R-79I16, genomic survey sequence.//3.3e-87:452:95//AQ283131

R-nnnnnnnnnnnnn

R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//0.50:256:61//AF068619

R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.//6.8e-62:320:96//AQ111163

R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.022:435:61//AC002476

R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//6.0e-56:660:71//AC002383

R-NT2RP4002905//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.0017:533:57//AL008972

R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934

R-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//2.1e-43:326:74//AC005510

R-OVARC1000006//HS_2253_B1_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=L, genomic survey sequence.//3.7e-35:191:98//AQ069124

R-OVARC1000013//HS_2212_A2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=12 Row=M, genomic survey sequence.//0.14:212:63//AQ210584

R-OVARC1000014//Human DNA sequence from PAC 463A9, on chromosome Xq25 contains STS.//0.0053:356:62//Z80232

R-OVARC1000017

R-OVARC1000035//RPCI11-65E1.TJ RPCI11 Homo sapiens genomic clone R-65E1, genomic survey sequence.//3.3e-05:236:63//AQ237194

R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and taga and tat repeat polymorphisms, complete sequence.//2.7e-48:325:82//AL008721

R-OVARC1000060//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.0e-21:297:70//AL033397

R-OVARC1000068//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.00038:553:58//X95276

R-OVARC1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.1e-110:599:93//AL031387

R-OVARC1000085//DNA encoding component HC5 of human proteasome.//2.7e-65:366:92//E03413

R-nnnnnnnnnnnnn//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.80:285:59//B94391

R-OVARC1000091

R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey sequence.//1.4e-17:141:85//AQ111520

R-OVARC1000106

R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//2.6e-100:495:97//AF069250

R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2.//9.5e-49:392:80//X71342

R-OVARC1000133//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//0.00020:243:65//U95740

R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q 25, complete sequence.//1.8e-16:370:67//AC005385

R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey sequence.//1.1e-05:55:98//AQ240492

R-OVARC1000151//M.musculus GEG-154 mRNA.//9.8e-21:192:81//X71642

R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 233 6F6, genomic survey sequence.//0.050:176:62//AQ042932

R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.7e-08:534:58//AC005506

R-OVARC1000198//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4 , BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.2e-11:556:96//AC004604

R-OVARC1000209//Blacus sp. 16S ribosomal RNA gene, partial sequence.//0. 55:165:67//AF003501

R-OVARC1000212//Mouse DNA for beta-casein.//0.56:225:63//X13484

R-OVARC1000240//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//6.2e-38:193:82//AC005670

R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//AF060194

R-OVARC1000288//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//5.4e- 07:128:70//D17131

R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//1.7e-10:100:88//AC005971

R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574

R-OVARC1000309

R-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.5e-83:453:94//AC005236

R-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1

C) mRNA, complete cds.//5.0e-58:455:81//U19614

R-OVARC1000335//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0483I23; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.034:429:60//AC005690

R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308

R-OVARC1000384//D.discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:62//M27588

R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:286:87//AD000812

R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720

R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3X10, genomic survey sequence.//1.8e-32:296:75//AG002388

R-OVARC1000420//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-48:354:77//AC005378

R-OVARC1000427//D.discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//X15382

R-OVARC1000431//HS_2199_A2_E02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=I, genomic survey sequence.//1.3e-34:186:98//AQ093722

R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662

R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:61//AC006043

R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381

R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1

.1e-77:418:94//AB014583

R-OVARC1000461//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417

R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.1e-81:489:91//AF023451

R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:72//AC004526.

R-OVARC1000473//Homo sapiens full length insert cDNA clone YI53C10.//3.2e-92:317:100//AF085851

R-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//2.7e-70:502:84//D87671

R-OVARC1000486//Dictyostelium discoideum Fusc (fusC) gene, partial cds./0.52:411:58//AF019984

R-OVARC1000496

R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from 22, complete sequence.//3.8e-17:294:71//AC005005

R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//4.5e-109:547:96//AC005024

R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.0e-46:264:93//AC004510

R-OVARC1000543//Caenorhabditis elegans cosmid F10C1.//0.00063:417:59//U49831

R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.5e-39:144:92//AL022069

R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complete sequence.//1.5e-81:429:96//AC005197

R-OVARC1000564//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.83:301:58//AC004223

R-OVARC1000573//Homo sapiens Xq28 genomic DNA in the region of the ALD 1 locus containing the genes for creatine transporter (SLC6A8), CDM, adreno leukodystrophy (ALD), Na⁺-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plex in related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq 28lul gene and cytochrome C (CCp) pseudogene.//2.4e-44:300:88//U52111

R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//6.4e-48:436:78//AF001549

R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//2.7e-32:313:78//AC005952

R-OVARC1000605

R-OVARC1000622//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//6.2e-43:328:83//AC006012

R-OVARC1000640//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.9e-47:514:73//AC005840

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//1.6e-29:162:100//AB011162

R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.50:270:60//AC005140

R-nnnnnnnnnnnnn//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.4e-83:549:86//AJ001713

R-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//3.2e-13:160:76//AL034424

R-OVARC1000689//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.90:230:61//U32943

R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//5.1e-15:133:85//AC005754

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130_H_16, complet

e sequence.//6.9e-48:525:73//AC005585
R-OVARC1000730//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00019:198:63//AQ093513
R-OVARC1000746//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:154:65//X95276
R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pTZ18R.//2.0e-30:187:78//M21185
R-OVARC1000771
R-OVARC1000781//Sequence 5 from Patent WO9722695.//8.4e-47:401:77//A63552
R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//7.8e-111:567:96//AC004542
R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds.//1.3e-17:119:95//L15189
R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBNL H171), complete sequence.//2.3e-51:482:78//AC005574
R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//3.6e-105:536:95//Y17711
R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//2.7e-107:538:96//AC004494
R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//3.6e-114:579:96//AF045584
R-OVARC1000862//M.musculus Fif mRNA.//2.3e-20:346:73//X71978
R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence.//9.1e-08:427:58//AE001416
R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//5.6e-34:357:78//U20086
R-OVARC1000885//Lycopersicon esculentum alcohol dehydrogenase homolog (G

AD3) mRNA; partial cds.//0.47:305:60//U21801

R-OVARC1000886

R-OVARC1000891//HS_3082_A2_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence.//1.1e-16:187:79//AQ122500

R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//7.2e-07:476:60//AL020989

R-OVARC1000912

R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1 Region, complete sequence.//1.6e-77:465:90//AC002471

R-OVARC1000936//HS_2195_A2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, genomic survey sequence.//2.4e-76:463:90//AQ191108

R-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//0.0028:161:65//Z99716

R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//3.5e-62:526:78//AB005549

R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products.//0.018:212:61//U61169

R-OVARC1000959//CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence.//1.1e-45:303:87//AQ111323

R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, complete sequence.//7.5e-44:353:81//AC005021

R-OVARC1000971//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//2.

2e-07:223:70//X91255

R-OVARC1000984

R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome 1q32. 1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicei n, Kalinin, BM600) and a novel Rat Ca2+/Calmodulin dependent Protein Kin ase LIKE gene. Contains ESTs, STSSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.//1.3e-06:179:70//AL023754

R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457_L_16, complet e sequence.//5.8e-71:332:87//AC003957

R-OVARC1001000//HS_3032_B1_G11_MF CIT Approved Human Genomic Sperm Libra ry D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey sequence.//5.1e-51:257:99//AQ096695

R-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete seque nce.//5.6e-92:473:96//AC004190

R-OVARC1001010//RPCI11-10P1.TV RPCI-11 Homo sapiens genomic clone RPCI-1 1-10P1, genomic survey sequence.//4.1e-05:201:65//B71813

R-OVARC1001011//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.9e-18:219:69//AC005520

R-OVARC1001032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c lone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464:86//AL022345

R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), com plete sequence.//1.4e-18:451:64//AC005220

R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.3e-99: 501:96//AF099149

R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096_G_20, comple te sequence.//9.7e-17:180:78//AC005410

R-OVARC1001044

R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal protein L41.//3.7e-15:124:88//Z12962

R-OVARC1001055//Homo sapiens, clone hRPK.15_A_1, complete sequence.//2.0e-30:292:76//AC006213

R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312:92//176237

R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.3e-95:463:98//AF082657

R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.92:272:59//U47276

R-OVARC1001074//HS_2205_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, genomic survey sequence.//1.3e-35:205:94//AQ184530

R-OVARC1001085

R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.5e-95:325:98//AJ005897

R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//1.0e-73:386:95//AF051782

R-OVARC1001117//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//6.1e-37:314:81//AC005272

R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBNL H73), complete sequence.//1.5e-44:390:77//AC005372

R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.//0.81:461:57//AJ235270

R-OVARC1001161//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342:64//AL031680

R-OVARC1001162//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//5.9e-48:347:85//B89781

R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.3e-28:427:70//AC004963

R-OVARC1001169//RPCI11-36P6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859

R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549

R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213

R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443K8 () complete sequence.//9.1e-41:516:72//AC005907

R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:134:85//AC004796

R-OVARC1001200//ALS=85 kda insulin-like growth factor binding protein-3 complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.12:345:60//S83462

R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:257:59//M36794

R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124_H_2, complete sequence.//1.4e-41:284:87//AC006071

R-OVARC1001243//HS_2055_B2_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey sequence.//0.59:83:75//AQ243142

R-OVARC1001261//Crocodylus porosus mRNA for transthyretin.//0.93:121:66//AJ223148

R-OVARC1001268

R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//0.0031:295:62//Z98551

R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-107:544:97//AC004494

R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPCI1-199J3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.025:402:59//AC00

6062

R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018

R-nnnnnnnnnnnn//Sequence 13 from patent US 5624818.//5.4e-85:577:84//I41142

R-OVARC1001329//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402

R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, complete sequence.//0.19:256:59//AC004862

R-OVARC1001339//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.5e-49:366:83//AC004242

R-OVARC1001341//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695020, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818

R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874

R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261j17 (LBNL H190), complete sequence.//2.8e-46:424:78//AC005350

R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//I34297

R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.786_0_4, complete sequence.//0.20:335:60//AC005863

R-OVARC1001369

R-OVARC1001372//S.scrofa DNA for myogenin 3' flanking region (285 bp).//6.9e-29:249:83//X89210

R-OVARC1001376//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.1e-50:491:73//AC004491

R-OVARC1001381//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//9.3e-20:422:60//AC005821

R-OVARC1001391

R-nnnnnnnnnnnnnnn

R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//9.9e-110:561:95/
/AB006651

R-OVARC1001419//CIT-HSP-2362F16.TR CIT-HSP Homo sapiens genomic clone 23
62F16, genomic survey sequence.//7.6e-47:242:98//AQ074668

R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete
sequence.//2.3e-20:211:66//AC005157

R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1.//0.18:148:
66//M80341

R-OVARC1001442

R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence.//
2.3e-19:181:81//AC002086

R-OVARC1001476//CITBI-E1-2517B6.TR CITBI-E1 Homo sapiens genomic clone 2
517B6, genomic survey sequence.//0.24:308:59//AQ278655

R-OVARC1001480//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 753D4, WORKING DRAFT SEQUENCE.//0.99:294:62//AL031676

R-OVARC1001489//E.caballus microsatellite DNA marker (clone ASB32).//0.8
7:81:71//X93546

R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete
cds.//9.3e-116:585:96//AF016507

R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 -c
omplete genomic sequence, complete sequence.//2.6e-40:285:86//AC002039

R-OVARC1001525//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3
unordered pieces.//1.0:320:59//AC006036

R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds.//5.0e-110:566:95//
AB016488

R-OVARC1001547

R-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseu

dogene.//5.9e-33:216:92//AF031165

R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//
AC002418

R-OVARC1001610//HS_3070_A2_A06_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3070 Col=12 Row=A, genomic survey
sequence.//0.47:107:66//AQ103523

R-OVARC1001611//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1185N5, WORKING DRAFT SEQUENCE.//0.17:236:63//AL034423

R-OVARC1001615//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 310013, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658

R-OVARC1001668//HS_3228_A2_E12_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3228 Col=24 Row=I, genomic survey
sequence.//4.6e-13:156:76//AQ188379

R-OVARC1001702//CITBI-E1-2501P16.TR.1 CITBI-E1 Homo sapiens genomic clon
e 2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965

R-OVARC1001703

R-OVARC1001711//CITBI-E1-2502N10.TF CITBI-E1 Homo sapiens genomic clone
2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194

R-OVARC1001726//CIT-HSP-232001.TF CIT-HSP Homo sapiens genomic clone 232
001, genomic survey sequence.//0.021:170:62//AQ038145

R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (p1).//2.5e-7
2:422:90//X05276

R-OVARC1001745//Human DNA sequence from clone 796I11 on chromosome 20q12
. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL
031257

R-nnnnnnnnnnnn//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete c
ds.//1.6e-08:396:60//M23166

R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eI
F3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6
 .3e-108:529:97//AB014575

R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence
 .//0.24:205:64//Z99279

R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequ
 ence.//4.6e-58:558:76//AC005066

R-OVARC1001795

R-OVARC1001802//Human HLA class III region containing cAMP response elem
 ent binding protein-related protein (CREB-RP) and tenascin X (tenascin-X
) genes, complete cds, complete sequence.//1.1e-37:346:78//U89337

R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.
 3-25.1. Contains the last coding exon of the gene for P18 component of a
 minoacyl-tRNA synthetase complex, part of an unknown gene downstream of
 a putative CpG island, and an STS with a CA repeat polymorphism, complet
 e sequence.//3.0e-112:581:95//AL023694

R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.2
 2-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, C
 K18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585

R-OVARC1001813//CITBI-E1-2508J18.TR CITBI-E1 Homo sapiens genomic clone
 2508J18, genomic survey sequence.//1.6e-72:386:95//AQ263046

R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//
 4.8e-41:320:83//AC002086

R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic
 sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.4e-08:527:58//A
 C004688

R-OVARC1001846//CIT-HSP-2014F15.TR CIT-HSP Homo sapiens genomic clone 20
 14F15, genomic survey sequence.//0.0045:165:67//B58905

R-OVARC1001861//M.musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X953

R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611

R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//9.1e-20:206:80//AL031864

R-OVARC1001880//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I15, genomic survey sequence.//3.9e-50:287:88//AQ052700

R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123_J_14, complete sequence.//6.1e-13:457:63//AC003950

R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.5e-86:346:90//AF061749

R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//7.2e-89:421:100//AF072246

R-OVARC1001911//Homo sapiens full length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315

R-OVARC1001916

R-OVARC1001928

R-OVARC1001942//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166

R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, envelope glycoprotein V3 region (env) gene, partial cds.//0.14:173:64//U58826

R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:63//M99593

R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//8.2e-38:385:75//AC005666

R-OVARC1001987

R-OVARC1001989//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **

* from clone Y57G11, WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841
R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.
2-24.3 Contains CpG island, complete sequence.//5.0e-42:298:86//AL031286
R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.
4e-107:542:96//AB007934
R-OVARC1002066//Arabidopsis thaliana chromosome II BAC F14M4 genomic seq
uence, complete sequence.//0.23:210:61//AC004411
R-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6
unordered pieces.//5.4e-99:546:92//AC006015
R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome Xq25-Xq
26. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), p
seudogene, ESTs.//4.4e-34:375:74//AL009174
R-OVARC1002127
R-OVARC1002138//CIT-HSP-2290018.TF CIT-HSP Homo sapiens genomic clone 22
90018, genomic survey sequence.//2.4e-07:316:62//AQ003988
R-OVARC1002143//RPCI11-54M8.TJ RPCI11 Homo sapiens genomic clone R-54M8,
genomic survey sequence.//2.3e-35:220:90//AQ083241
R-OVARC1002156
R-OVARC1002158//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2
514D4, genomic survey sequence.//1.6e-12:140:79//AQ265720
R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP Homo sapiens genomic clone 230
7C9, genomic survey sequence.//5.0e-59:291:99//AQ020420
R-OVARC1002182//P. falciparum SD17 gene for knob-associated histidine-ri
ch protein.//0.74:161:65//Y00060
R-PLACE1000004//D.discoideum gene for protein kinase.//0.00081:263:59//Z
37981
R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 geno
mic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58
//AC005507

R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97/
/AF070557

R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, p1 clone:
T1212 and T1601, WORKING DRAFT SEQUENCE.//2.8e-44:405:77//D83253

R-PLACE1000031//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequ
ence.//1.8e-24:291:73//AC006162

R-PLACE1000040//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y105C5, WORKING DRAFT SEQUENCE.//0.00039:289:61//Z98855

R-PLACE1000048//Human BAC clone RG210I04, complete sequence.//4.7e-83:51
8:89//AC002462

R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic
sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.98:73:76//AC00
5505

R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125
:98//L22154

R-PLACE1000066

R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKIN
G DRAFT SEQUENCE, 6 unordered pieces.//1.2e-87:456:95//AC005848

R-PLACE1000081

R-PLACE1000094//RPCI11-91K6.TV RPCI11 Homo sapiens genomic clone R-91K6,
genomic survey sequence.//2.3e-83:409:98//AQ282619

R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746_E_8, complete
sequence.//1.8e-06:420:57//AC005358

R-PLACE1000142

R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, compl
ete cds.//1.3e-112:594:94//AF058291

R-PLACE1000185

R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 23
08A18, genomic survey sequence.//8.2e-80:410:97//AQ022149

R-PLACE1000214//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
 from contig 3-09, complete sequence.//1.6e-05:548:59//AL008989

R-PLACE1000236//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
 lone 695020, WORKING DRAFT SEQUENCE.//2.2e-16:118:91//AL032818

R-PLACE1000246//X.laevis mRNA for XLCL2 protein.//6.5e-13:66:95//Z14122

R-PLACE1000292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
 lone 111B22, WORKING DRAFT SEQUENCE.//6.6e-41:322:84//Z98200

R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281_F_24, complet
 e sequence.//1.8e-16:598:62//AC004706

R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete
 sequence.//2.3e-11:237:69//AC005326

R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, co
 mplete sequence.//8.7e-09:492:58//AC005278

R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 73 of t
 he complete sequence.//0.59:354:59//AE001364

R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtmr1) mRNA
 , complete cds.//0.55:65:84//AF073997

R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 u
 nordered pieces.//3.6e-17:152:83//AC005015

R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon
 e: K21H1, complete sequence.//0.51:346:58//AB020742

R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr
 ome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP00
 0009

R-PLACE1000421//HS_2251_B2_G12_MR CIT Approved Human Genomic Sperm Libra
 ry D Homo sapiens genomic clone Plate=2251 Col=24 Row=N, genomic survey
 sequence.//1.4e-82:430:95//AQ192807

R-PLACE1000424//Human PAC clone DJ515N1 from 22q11.2-q22, complete seque
 nce.//1.8e-36:483:71//AC002073

R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence.//2.6e-37:371:76//AF015724

R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227_G_15, complete sequence.//1.0e-54:429:81//AC005899

R-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//0.66:103:72//AF059580

R-PLACE1000481//Human DNA sequence from clone 960017 on chromosome Xp11.21-11.22 Contains EST, CA repeat(DXS991), STS, GSS, complete sequence.//0.019:171:66//AL022166

R-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//3.2e-17:221:72//U35245

R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00045:480:60//AC005308

R-PLACE1000547//Homo sapiens chromosome 19, cosmid F17987, complete sequence.//9.6e-32:231:85//AC004790

R-PLACE1000562//, complete sequence.//1.8e-45:280:92//AC005409

R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302

R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799_N_11, complete sequence.//1.5e-37:414:74//AC005323

R-nnnnnnnnnnnnn//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//1.9e-77:542:82//M55542

R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00019:482:59//AC005506

R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1

A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3)./
/5.6e-51:369:85//U66059

R-PLACE1000610//HS_3071_A1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341

R-PLACE1000636//HS_3220_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey sequence.//0.010:253:64//AQ181157

R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:96//AF102265

R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896

R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219

R-PLACE1000712//Homo sapiens full length insert cDNA clone ZD76G10.//1.0e-69:345:98//AF086408

R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//1.0:174:62//AC002300

R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547

R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791

R-PLACE1000755//HS_2183_B1_H11_MF CIT Approved Human Genomic Sperm Library

ry D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202

R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.0e-38:492:74//AC004847

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548

R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds.//0.078:180:68//U58970

R-nnnnnnnnnnnnn

R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1./5.1e-26:348:72//AF039904

R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//1.4e-26:110:95//U02081

R-nnnnnnnnnnnnn//Homo sapiens full length insert cDNA clone ZD55D10.//1.4e-13:93:96//AF086334

R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//2.7e-09:484:59//L04272

R-PLACE1000863

R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//AC005505

R-PLACE1000931//RPCI11-66P7.TK RPCI11 Homo sapiens genomic clone R-66P7, genomic survey sequence.//3.4e-73:369:97//AQ237489

R-PLACE1000948//RPCI11-64K15.TK RPCI11 Homo sapiens genomic clone R-64K15, genomic survey sequence.//6.6e-06:258:62//AQ239337

R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//8.3e-20:223:76//AC005553

R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00030:448:59//AC005506

R-PLACE1000979

R-PLACE1001000//CIT-HSP-2297I8.TF CIT-HSP Homo sapiens genomic clone 2297I8, genomic survey sequence.//7.0e-07:64:95//AQ004997

R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds.//0.0078:215:64//D26607

R-PLACE1001010

R-PLACE1001015//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.5e-16:452:63//AL022318

R-PLACE1001024//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//0.99:186:63//AL024498

R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-15:313:68//AC005377

R-PLACE1001062//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.3e-16:119:84//AC003664

R-PLACE1001076

R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696

R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07:302:62//AC005139

R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372

R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6 q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSS, complete sequence.//4.9e-06:334:60//Z84480

R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412

R-PLACE1001168//HS_2036_A1_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=0, genomic survey sequence.//0.40:144:63//AQ230662

R-PLACE1001171

R-PLACE1001185

R-PLACE1001238//Human coxVIb gene, last exon and flanking sequence.//3.4e-36:349:76//X58139

R-PLACE1001241//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.11:258:61//AL008972

R-PLACE1001257//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B4P3; HTGS phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016

R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//AF045448

R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839

R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 2328B24, genomic survey sequence.//5.4e-24:147:76//AQ042129

R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642

R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//AC003682

R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286

R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSS, complete sequence.//7.2e-39:308:83//Z84480

R-PLACE1001351//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399
R-PLACE1001366//Human Na⁺/phosphate co-transporter gene, exon 1, partial
sequence.//2.2e-46:369:82//D89927
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-8
0:431:93//AF009615
R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97/
/AF055030
R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86
:456:94//AJ001319
R-PLACE1001387
R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence
.//0.054:148:68//U95355
R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING
DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412
R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence./
/8.0e-44:242:95//AF091087
R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete
sequence.//0.12:53:84//AC006241
R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD 1
ocus containing the genes for creatine transporter (SLC6A8), CDM, adreno
leukodystrophy (ALD), Na⁺-isocitrate dehydrogenase gamma subunit (IDH),
and translocon-associated protein delta (TRAP) genes, complete cds, plex
in related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq
28lul gene and cytochrome C (CCp) pseudogene.//1.0:250:61//U52111
R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete
genome.//0.0077:173:62//AE001130
R-PLACE1001468//HS_3050_A2_D07_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey

sequence.//0.00023:202:65//AQ133920

R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.2e-17:180:80//AC002368

R-PLACE1001502//RPCI11-24F2.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24F2, genomic survey sequence.//0.15:203:66//B84401

R-PLACE1001503//HS_2183_A1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey sequence.//1.3e-38:181:82//AQ022613

R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds.//6.4e-56:339:90//AB006969

R-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667

R-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence.//2.6e-18:171:82//AC005669

R-PLACE1001551

R-PLACE1001570//M.capricolum DNA for CONTIG MC188.//0.0043:305:57//Z33135

R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//2.5e-82:408:98//AB020860

R-PLACE1001603//Homo sapiens KE05 protein mRNA, complete cds.//1.5e-40:295:84//AF064605

R-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.5e-39:307:82//AC005037

R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.9e-41:217:97//AF054174

R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds.//1.4e-08:178:65//M27878

R-PLACE1001634//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **

* from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791
R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete
sequence.//2.6e-83:441:95//AC005971
R-PLACE1001672//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA2
6H8.//0.91:115:69//Z79253
R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48
-18) mRNA, complete cds.//1.5e-111:545:97//AF069250
R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 u
nordered pieces.//1.0e-46:478:75//AC005077
R-PLACE1001705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716
R-PLACE1001716//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Ca
ncer Center) complete sequence.//0.96:172:66//AC002349
R-PLACE1001720
R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cd
s.//0.79:280:60//U31120
R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete seq
uence.//1.0:109:65//AC005261
R-PLACE1001740//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete
sequence.//5.3e-11:249:67//AC006027
R-PLACE1001745
R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complet
e sequence.//6.0e-05:337:61//AC005509
R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.
//1.3e-91:540:89//AF061243
R-PLACE1001756//Human BAC clone RG302F04 from 7q31, complete sequence.//
0.074:344:62//AC002463
R-PLACE1001761
R-PLACE1001771//Homo sapiens full length insert cDNA clone ZD79C11.//4.4

e-57:298:96//AF086426

R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Tt819.//4.6e-05:282:61//M15711

R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.015:331:58//AC004710

R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//4.1e-92:463:95//AF058953

R-PLACE1001821//***ALU WARNING: Human Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567

R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds.//9.1e-26:313:73//U37351

R-PLACE1001869

R-PLACE1001897//Mus musculus homeobox protein (Dlx5) mRNA, complete cds.//0.0043:207:64//AF033011

R-PLACE1001912//RPCI11-25F23.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25F23, genomic survey sequence.//6.3e-33:248:67//AQ013567

R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//5.0e-73:363:98//AF070671

R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//0.98:248:60//AC005245

R-PLACE1001983//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y40H7, WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389

R-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.4e-44:376:80//AL023755

R-PLACE1002046//CITBI-E1-2520J24.TF CITBI-E1 Homo sapiens genomic clone 2520J24, genomic survey sequence.//4.5e-20:144:89//AQ280117

R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers DXS366 and DXS87 on chromosome X contains STS.//0.025:362:57//Z80900

R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:1
97:62//X02438

R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), c
omplete sequence.//9.7e-06:414:60//AC004763

R-PLACE1002073

R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -
complete genomic sequence, complete sequence.//1.8e-06:278:63//AC002302

R-PLACE1002115//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone Y214H10, WORKING DRAFT SEQUENCE.//6.0e-12:327:64//AL022344

R-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//5.1e-67:44
2:86//AF079527

R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome X
q25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome pr
oteins OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:
403:97//AL022162

R-PLACE1002150//Human DNA sequence from PAC 145B12 on chromosome Xq27-Xq
28. Contains EST, CA repeat and STS.//0.043:455:59//AL008706

R-PLACE1002157//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.
2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrie
r family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium
-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849

R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA 1 allele) ge
ne, exon 2, partial cds.//0.82:96:70//U44785

R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete seq
uence.//0.83:196:65//AC004456

R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome Xp22.11
-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and
the first coding exon of the RS1 gene for retinoschisis (X-linked, juve
nile) 1 (XLRIS1). Contains ESTs, an STS and GSSs, complete sequence.//0.0

017:193:61//Z94056

R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//AC004152

R-PLACE1002227//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:80//AC003071

R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-06:478:57//AC004907

R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255

R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00023:549:58//AC005505

R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271

R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//AC005329

R-PLACE1002399//Human HepG2 3' region cDNA, clone hmd5d06.//2.4e-71:411:92//D16939

R-PLACE1002433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//0.85:176:63//AL031984

R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence.//0.0040:213:63//AC002542

R-PLACE1002438//CITBI-E1-2501M20.TF.1 CITBI-E1 Homo sapiens genomic clone 2501M20, genomic survey sequence.//0.70:247:61//AQ242104

R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3.//0.00060:471:59//AJ229041

R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//2.5e-10:98:81//AC004854

R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1

.7e-25:199:71//U69262

R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSS. Contains polymorphic CA repeat.//1.2e-11:382:63//Z92545

R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.1e-53:307:91//AF042273

R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence.//0.56:270:60//Z98551

R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey sequence.//3.2e-42:297:85//AQ037614

R-PLACE1002514//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//7.8e-16:221:73//Z95114

R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.6e-86:582:85//AB018256

R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97//AC004774

R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.//0.0042:489:60//D16253

R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178

R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//2.5e-44:292:84//AC006084

R-PLACE1002583//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//3.1e-17:517:61//AF045555

R-PLACE1002591

R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence.//0.080:308:60//AL032626

R-PLACE1002604//Human cosmid LL12NC01-88A9, ETV6 gene, exons 6, 7 and 8

and partial cds.//0.0013:176:65//U63313

R-PLACE1002625//HS_2233_B2_H04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663

R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-46:272:94//AF079765

R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-77:390:97//AF068180

R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656

R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//I73723

R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library) complete sequence.//0.0098:197:64//AC005185

R-PLACE1002772//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//6.7e-49:378:82//AC006145

R-PLACE1002782

R-PLACE1002794

R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey sequence.//6.0e-50:250:100//AQ034981

R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279

R-PLACE1002816//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-59:339:93//AC004466

R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-78:413:95//M27877

R-PLACE1002839//Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.//6.5e-25:301:74//AC004819

R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey sequence.//0.0011:210:61//AQ040519

R-PLACE1002853//Human interleukin 6 (IL6) gene, 3' flank.//5.8e-06:327:61//J03049

R-PLACE1002881

R-PLACE1002908//HS_3064_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence.//1.9e-09:156:72//AQ142985

R-PLACE1002941

R-PLACE1002962

R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721

R-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755

R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.//0.56:88:72//AC004921

R-PLACE1002996//HS_2064_A1_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211

R-PLACE1003025//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//0.26:428:58//AC006145

R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.3e-95:465:98//AC005920

R-PLACE1003044

R-PLACE1003092//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266

R-PLACE1003100//HS_2244_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=0, genomic survey sequence.//2.3e-42:288:86//AQ084224

R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00066:233:61//AC004885

R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence.//0.019:429:57//AL034558

R-PLACE1003145

R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//3.2e-05:390:58//AC004616

R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone : MTE17, complete sequence.//2.4e-06:390:60//AB015479

R-PLACE1003176

R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-78:406:81//AC005095

R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence.//0.016:411:57//Z98551

R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00084:288:61//AC005139

R-PLACE1003238//Homo sapiens full length insert cDNA clone ZD79H11.//7.6e-114:567:96//AF086432

R-PLACE1003249//Human Chromosome X, complete sequence.//1.3e-45:317:85//AC002416

R-PLACE1003256//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//1.0e-45:328:85//AC004099

R-PLACE1003258

R-PLACE1003296//Diphoropria sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.//0.050:228:59//U39952

R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.7e-91:458:96//M27877

R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 2 2q13-q13.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuclear pore complex protein Npap60). Contains ESTs, complete sequence.//4.3e-34:370:71//Z82243

R-PLACE1003342//CIT-HSP-2311D21.TF CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence.//1.0:159:68//AQ020460

R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-05:330:61//AC004153

R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//3.4e-98:469:98//U92715

R-PLACE1003361

R-PLACE1003366//Homo sapiens CAG repeated sequence.//0.018:319:61//AJ006805

R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence.//0.050:155:63//B20174

R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence.//1.2e-62:434:83//AC004771

R-PLACE1003375//Dictyostelium discoideum golvesin (gol) gene, complete cds.//0.042:263:57//U89350

R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//1.7e-83:429:96//AB020878

R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//2.4e-13:175:76//AC005695

R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete

sequence.//2.1e-05:340:61//AC005587
R-PLACE1003454//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from contig 3-64, complete sequence.//0.47:411:58//AL009014
R-PLACE1003478//M.capricolum DNA for CONTIG MC175.//0.51:253:59//Z33125
R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete
sequence.//4.6e-37:319:81//AC006080
R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 22
95M19, genomic survey sequence.//1.0e-40:251:90//AQ007480
R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequ
ence, containing ribosomal protein homologue pseudogene L23a.//2.7e-29:1
63:89//AF064859
R-PLACE1003521//HS_3252_A2_G05_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic survey
sequence.//0.00017:274:60//AQ221562
R-PLACE1003528//HS_2041_B1_B07_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey
sequence.//6.6e-40:219:83//AQ230483
R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxida
se subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) g
enes, and unidentified reading frames A61, 2 and 3.//8.3e-05:300:61//J01
404
R-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 97P20, WORKING DRAFT SEQUENCE.//2.7e-87:450:96//AL031297
R-PLACE1003566
R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete
sequence.//4.7e-20:148:78//AC003965
R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.
//3.5e-18:287:68//Z99571
R-PLACE1003584

R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence./
/2.5e-10:153:73//AF061032

R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence./
6.9e-07:240:65//AC002066

R-PLACE1003596//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y87G2, WORKING DRAFT SEQUENCE.//0.13:393:60//AL022597

R-PLACE1003602//Homo sapiens mRNA expressed in placenta.//2.4e-95:576:88
//D83200

R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequ
ence.//2.9e-19:302:71//AC002081

R-nnnnnnnnnnnnn

R-PLACE1003618//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 191E19, WORKING DRAFT SEQUENCE.//8.3e-57:469:80//AL034451

R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic
sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.1e-05:339:62//A
C004688

R-PLACE1003638//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1104E15, WORKING DRAFT SEQUENCE.//2.5e-38:279:84//AL022312

R-PLACE1003669//HS_3054_A2_E07_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3054 Col=14 Row=I, genomic survey
sequence.//0.014:265:61//AQ132713

R-PLACE1003704//HS_3213_A1_D12_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3213 Col=23 Row=G, genomic survey
sequence.//0.80:195:61//AQ176784

R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequenc
e.//0.018:152:61//AC002067

R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete c
ds.//1.7e-61:366:89//D26607

R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome

22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//2.7e-44:505:73/AL022336

R-PLACE1003738//H.sapiens DNA sequence.//0.93:185:60//Z22357

R-PLACE1003760//Human globin gene.//5.9e-97:538:91//M69023

R-PLACE1003762//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//4.6e-13:134:79//AC003070

R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//5.4e-12:189:71//AC005919

R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//1.7e-119:619:95//AC004160

R-PLACE1003783

R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.//5.6e-15:204:74//AC004659

R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//7.0e-37:234:89//AQ114933

R-PLACE1003833//Homo sapiens full length insert cDNA clone ZE15C06.//4.4e-59:313:95//AF086558

R-PLACE1003850

R-PLACE1003858

R-PLACE1003864

R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 In DG CR Region, complete sequence.//8.7e-33:285:81//AC000072

R-nnnnnnnnnnnnn

R-PLACE1003886

R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//0.73:127:65//AC004069

R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//1.9e-05:239:59//L78810

R-PLACE1003903//Homo sapiens full length insert cDNA clone ZD78D11.//8.1e-74:369:97//AF086422

R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.//0.56:247:61//U73520

R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.67:213:63//Z99281

R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//8.7e-49:342:85//Z74022

R-PLACE1003936//H.sapiens gene for ventricular myosin light chain 2.//2.6e-09:394:61//Z15030

R-PLACE1003968//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-62, complete sequence.//1.3e-07:245:65//AL010247

R-PLACE1004104

R-PLACE1004114//Human PAC clone RG212D03, complete sequence.//5.0e-07:336:61//AC002485

R-PLACE1004118//HS_3092_B1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=1 Row=D, genomic survey sequence.//0.80:207:60//AQ128151

R-PLACE1004128//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//1.8e-06:193:66//AF022085

R-PLACE1004149//HS_2253_A2_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=22 Row=K, genomic survey sequence.//2.4e-59:315:95//AQ129711

R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.3e-53:299:76//AC005295

R-PLACE1004161

R-PLACE1004183//Homo sapiens for TOM1-like protein.//1.3e-80:434:93//AJ010071

R-PLACE1004197//RPCI11-69N15.TK RPCI11 Homo sapiens genomic clone R-69N15, genomic survey sequence.//0.0078:170:65//AQ265515

R-PLACE1004203//Homo sapiens semaphorin L (SEMAL) mRNA, complete cds.//3.4e-105:501:98//AF030698

R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6 q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//6.1e-65:373:86//AL021326

R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.011:383:61//AC006031

R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.4e-09:576:59//AC004470

R-PLACE1004258//HS_3034_A1_B12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=23 Row=C, genomic survey sequence.//1.4e-35:359:77//AQ128936

R-PLACE1004270//CITBI-E1-2504K14.TR CITBI-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108

R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//0.025:116:72//AC005234

R-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//4.4e-106:581:91//AF084830

R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.59:231:60//AC005308

R-PLACE1004289//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//5.8e-31:340:75//AC005920

R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.4e-90:572:86//AC005095

R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//1.9e-113:590:94//Y11588

R-PLACE1004336//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033383

R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//2.4e-70:379:93//AF100153

R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clone 2287M8, genomic survey sequence.//0.47:173:61//AQ000837

R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic clone 2316J11, genomic survey sequence.//0.035:109:69//AQ037817

R-PLACE1004388//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-82, complete sequence.//4.2e-06:381:60//AL010149

R-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.20:270:60//AC005027

R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-pl3, complete sequence.//1.3e-96:516:94//AC005532

R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, complete sequence.//5.8e-10:279:65//AL031296

R-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.9e-88:516:88//U49283

R-PLACE1004451//HS_2258_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, genomic survey sequence.//0.82:172:61//AQ221189

R-PLACE1004460

R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspartate transcarbamylase-dihydroorotase (CAD) gene, exons 1 and 2.//1.2e-24:311:62//M31621

R-PLACE1004471//Homo Sapiens Chromosome X clone bWxD75, complete sequence.//2.1e-34:333:70//AC004389

R-PLACE1004473

R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T region.//1.0e-08:485:60//U11584

R-PLACE1004506

R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427

R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071

R-PLACE1004518

R-PLACE1004548//Homo sapiens Xp22 BAC GS-551019 (Genome Systems Human BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride channel 4 gene, complete sequence.//4.9e-40:245:80//AC003666

R-PLACE1004550

R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.7e-82:532:86//X75931

R-PLACE1004629//Homo sapiens chromosome 7 clone UWGC:g3586a230 from 7p14-15, complete sequence.//0.015:437:59//AC004800

R-PLACE1004645//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.033:76:75//AQ110136

R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28, complete sequence.//2.0e-23:237:79//AF036876

R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPCI11-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.1e-09:94:87//AC005343

R-nnnnnnnnnnnn//RPCI11-79G23.TV RPCI11 Homo sapiens genomic clone R-79G23, genomic survey sequence.//2.2e-81:433:94//AQ283692

R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263:74//U07561

R-PLACE1004674//Homo sapiens calcium binding protein. (ALG-2) mRNA, complete cds.//1.1e-89:513:91//AF035606

R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//1.3e-96:498:95//AB020860

R-PLACE1004686

R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 2/11.//2.1e-33:290:80//AB020859

R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequence.//1.0:195:60//AL021448

R-PLACE1004716//CITBI-E1-2519C14.TR CITBI-E1 Homo sapiens genomic clone 2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965

R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0022:360:60//AC005507

R-PLACE1004736

R-PLACE1004740

R-nnnnnnnnnnnnn//Homo sapiens ubiquitin-protein ligase E3-alpha (UBR1) mRNA, partial cds.//5.4e-105:575:92//AF061556

R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//9.0e-26:317:76//AC002523

R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//8.5e-88:437:96//AF084367

R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:138:65//AP000010

R-PLACE1004793//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR./

/5.1e-58:313:80//U60269

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.8e-98:580:88//AB011178

R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140

R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-107:358:99//AF069250

R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//3.8e-61:353:89//AC004126

R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666

R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC00366

9

R-PLACE1004836//HS_2270_A2_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=0, genomic survey sequence.//8.6e-51:267:96//AQ164110

R-PLACE1004838//CIT-HSP-2343E10.TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544

R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//I928
20

R-PLACE1004868//Human Chromosome X clone bW XD342, complete sequence.//0.57:344:59//AC004072

R-PLACE1004885//HS_3235_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193

R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related

, matrix associated, actin dependent regulator of chromatin, subfamily a
, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains
ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577

R-PLACE1004902

R-PLACE1004913//Human DNA sequence from clone J428A131, WORKING DRAFT SE
QUENCE.//7.7e-58:377:87//Z82209

R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, c
omplete sequence.//0.00084:373:60//AC004605

R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0
e-100:532:93//AF099936

R-PLACE1004934//Homo sapiens clone RG062N11, WORKING DRAFT SEQUENCE, 2 u
nordered pieces.//0.00030:198:66//AC005683

R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cd
s.//1.3e-13:367:61//AF020788

R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, com
plete sequence.//0.97:116:71//Z84494

R-PLACE1004972

R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:3
04:60//AL008970

R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic
sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//
AC005308

R-PLACE1004985//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522

R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complet
e sequence.//2.7e-56:158:99//AC004925

R-PLACE1005027

R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequ
ence.//3.1e-63:438:86//AC005775

R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867

R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSS and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584

R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556

R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293_K_20, complete sequence.//2.1e-42:384:69//AC005495

R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey sequence.//0.13:112:67//B87788

R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401

R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476

R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195

R-PLACE1005111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845

R-PLACE1005128

R-PLACE1005146

R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140

R-PLACE1005176//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018

R-PLACE1005181//HS_2182_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey

sequence.//4.9e-05:193:65//AQ030787
R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161
R-PLACE1005206//Homo sapiens full length insert cDNA YN66A06.//6.3e-64:343:93//AF075043
R-PLACE1005232//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476
R-PLACE1005243
R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132
R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067
R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720
R-PLACE1005287//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744
R-PLACE1005305//HS_3180_B2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443
R-PLACE1005308
R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.00048:320:60//AC000383
R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537:94//AB007960
R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//2.2e-94:536:91//AC004794
R-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.3e-32:313:79//AC000380
R-PLACE1005373//Homo sapiens BAC129, complete sequence.//8.8e-10:229:68/

/U85195

R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//3.0e-44:434:77//AC005291

R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//8.8e-105:529:96//AC003991

R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.7e-39:302:82//AC002477

R-PLACE1005467//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19, WORKING DRAFT SEQUENCE.//1.1e-40:328:81//Z93014

R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//6.4e-68:409:90//AL022310

R-PLACE1005477//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//0.020:216:66//AL023693

R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//2.8e-44:327:70//AC005392

R-PLACE1005481//Homo sapiens chromosome 17, clone hRPC.1164_0_3, complete sequence.//4.2e-23:284:74//AC004703

R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4.//0.19:468:60//AF031631

R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.6e-55:277:98//AF071185

R-PLACE1005526//Human mRNA for alpha-1 type II collagen.//0.10:227:63//X16468

R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.3e-76:395:96//AP000038

R-PLACE1005530//C.familiaris CA repeat sequence (isolate).//0.023:90:75
//X86184

R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence.//2.0e-09:235:64//AL025928

R-PLACE1005554//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.//0.069:305:60//AC005969

R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//4.3e-105:587:91//AC004707

R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequence.//1.5e-17:274:67//AC003971

R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//2.7e-15:191:77//AC004991

R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//6.4e-90:453:96//AC004126

R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence.//0.69:322:61//U72788

R-PLACE1005611//Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds.//0.059:473:56//U42599

R-PLACE1005623//Homo sapiens full length insert cDNA clone ZD76B03.//1.6e-113:575:95//AF086405

R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-79:270:94//AC005840

R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequence.//8.2e-56:441:83//AC002382

R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//3.2e-110:585:93//AF083255

R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//8.6e-08:505:58//AC005701

R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X conta

ins EST, CpG island and polymorphic CA repeat.//3.2e-27:307:72//Z82203
R-PLACE1005698//344B22.TV CIT978SKA1 Homo sapiens genomic clone A-344B22
, genomic survey sequence.//0.030:91:70//B15144
R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele
e 17R1 3' to collagen type II (COL2A1) gene.//5.2e-10:587:59//L10171
R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete
cds.//0.0039:239:58//L78810
R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds
.//2.2e-21:270:72//U15635
R-PLACE1005755//Caenorhabditis elegans cosmid M03F4.//6.9e-08:219:64//U6
4601
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds.//1.0e-45:268:
87//D42087
R-PLACE1005799//Human X chromosome mRNA for CCG1 protein inv. in cell pro
liferation.//0.030:91:78//X07024
R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequ
ence.//1.4e-69:391:92//AC004827
R-PLACE1005803
R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete sequenc
e.//1.8e-21:175:75//AC002530
R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING
DRAFT SEQUENCE, 1 ordered pieces.//2.9e-56:333:91//AC004150
R-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from MAL1P2, WORKING DRAFT SEQUENCE.//0.020:513:55//AL031745
R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8e-10:18
2:69//Y00763
R-PLACE1005850
R-PLACE1005851//Homo sapiens clone DJ0789I05, WORKING DRAFT SEQUENCE, 2
unordered pieces.//5.5e-06:318:63//AC004887

R-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//6.7e-28:366:72//X75931

R-PLACE1005884//Human DNA sequence from cosmid V526F1, between markers DXS366 and DXS87 on chromosome X contains STS.//1.0e-06:306:64//Z70281

R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0094:449:59//AC005139

R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone 2509N21, genomic survey sequence.//4.8e-84:494:89//AQ261347

R-PLACE1005923//RPCI11-65N9.TJ RPCI11 Homo sapiens genomic clone R-65N9, genomic survey sequence.//8.3e-97:520:93//AQ237243

R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//5.2e-67:578:78//AL022719

R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete sequence.//0.0035:176:62//AL032654

R-PLACE1005934

R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence.//0.00021:272:62//AF069716

R-PLACE1005951

R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349:60//U37429

R-PLACE1005955//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//8.3e-08:128:70//D17131

R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//7.0e-09:549:59//AF044863

R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1e-51:394:81//AB002086

R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//4.4e-63:369:91//AC005866

R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//5.9e-27:299:74//U15177

R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequence.//3.5e-07:164:67//AF046375

R-PLACE1006011//Mus musculus poly-(ADPribosyl)-transferase homolog PARP mRNA, complete cds.//1.1e-32:266:83//AF072521

R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e In DGCR Region, complete sequence.//1.8e-17:164:82//AC000077

R-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//2.0e-49:557:72//U01139

R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13:128:81//X99906

R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.3e-18:220:74//AC004885

R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, complete CDS.//0.0050:271:63//AJ005122

R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//0.43:178:65//AC005454

R-PLACE1006139//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.5e-13:222:68//AC004849

R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence.//0.00019:455:59//Z98551

R-PLACE1006157//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.00018:351:60//AL034557

R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01_124_D_3 map 10 q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.0e-113:586:96//AC006103

R-PLACE1006164//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.0e-28:342:75//U91328

R-PLACE1006167//Homo sapiens full length insert cDNA clone ZE14E04.//4.6e-77:426:93//AF086555

R-nnnnnnnnnnnnn//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82//X14972

R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-116:597:95//AF091433

R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete sequence.//8.8e-11:148:74//AC004410

R-PLACE1006196

R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.//8.4e-44:332:85//AC000398

R-PLACE1006223//Human DNA sequence from cosmid U74C11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.041:215:61//Z73362

R-PLACE1006225//Caenorhabditis elegans cosmid Y69H2, complete sequence.//9.7e-13:358:63//Z98877

R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.//0.00019:538:58//AL008970

R-nnnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//3.1e-96:497:95//AC004142

R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.029:499:56//AC006034

R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//9.2e-96:499:95//AB014548

R-PLACE1006262//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//0.00043:160:66//AC004087

R-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20N2, WORKING DRAFT SEQUENCE.//3.5e-120:611:96//AL031320

R-PLACE1006318

R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.//1.0:426:57//AL034560

R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq21.//0.96:173:66//AL008987

R-PLACE1006357//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.9e-07:491:58//X95276

R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:56//AE001398

R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence.//1.0:240:59//AL031630

R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//3.7e-101:574:91//AC004232

R-PLACE1006382

R-PLACE1006385//Mus musculus intersectin-EH binding protein Ibp2 mRNA, partial cds.//1.4e-50:350:86//AF057286

R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//5.1e-51:339:82//AC004854

R-PLACE1006414//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-38:297:84//AC004804

R-PLACE1006438//Homo sapiens full length insert cDNA YH73H06.//7.6e-73:422:90//AF074985

R-PLACE1006445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE.//3.0e-07:376:61//AL031726

R-PLACE1006469

R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152

R-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//3.0e-101:535:94//AL021977

R-PLACE1006492//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//0.78:44:95//AC005972

R-PLACE1006506//R.norvegicus BSP gene.//1.0:206:60//X86100

R-PLACE1006521//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//9.0e-17:414:61//B75158

R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7.//0.98:186:63//AJ002197

R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934

R-PLACE1006540//Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.//7.5e-41:470:70//AC004209

R-PLACE1006552//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS ** * from clone Y47D3, WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865

R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.016:291:58//AC004710

R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//2.9e-116:590:95//U97670

R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.2e-45:209:88//AC004050

R-PLACE1006626//C. elegans cosmid K12H4.//1.2e-16:344:64//L14331

R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//2.8e-25:343:70//AC006128

R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence.//0.00020:201:62//B90038

R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-42:309:84//AC004882

R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence.//6.4e-09:454:59//AC006024

R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, complete sequence.//0.56:226:63//AL022154

R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence.//6.0e-101:486:98//AF038172

R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.4e-68:381:93//AC005626

R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence.//6.2e-72:397:92//AF070622

R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds.//1.6e-11:420:61//U20984

R-PLACE1006782//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.60:321:58//Z98865

R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//2.9e-40:379:77//AC005599

R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//6.2e-07:291:63//AC005083

R-PLACE1006800//HS_2270_B1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence.//4.1e-76:367:99//AQ085793

R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00058:354:59//AC005507

R-PLACE1006815//HS_3028_B1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence.//1.5e-33:251:77//AQ120174

R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat

t, CpG island, CpG island genomic fragments.//1.4e-76:544:84//Z86062
R-PLACE1006829
R-PLACE1006860
R-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 323M4, WORKING DRAFT SEQUENCE.//3.2e-107:549:95//AL033378
R-PLACE1006878//Homo sapiens full length insert cDNA clone ZB55G05.//1.4
e-46:241:97//AF086155
R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), c
omplete sequence.//1.3e-38:283:85//AC004232
R-nnnnnnnnnnnnn
R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X conta
ins EST, CpG island and polymorphic CA repeat.//4.1e-15:477:62//Z82203
R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Sys
tems Human BAC Library) complete sequence.//1.3e-42:305:87//AC005184
R-PLACE1006932
R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X.//0.0
014:114:74//Z86061
R-nnnnnnnnnnnnn//Mouse mRNA for germ cell specific protein APG-1, complet
e cds.//9.5e-85:590:83//D49482
R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete
sequence.//6.7e-42:295:86//AC005544
R-PLACE1006962//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Ca
ncer Center) complete sequence.//1.1e-19:302:71//AC002349
R-PLACE1006966//HS_2219_B2_C02_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=2219 Col=4 Row=F, genomic survey s
equence.//0.019:180:63//AQ145873
R-PLACE1006989
R-PLACE1007014
R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORK

ING DRAFT SEQUENCE, 48 unordered pieces.//1.6e-23:362:70//AC005845
R-PLACE1007045//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 32B1, WORKING DRAFT SEQUENCE.//2.3e-90:584:86//AL023693
R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8
unordered pieces.//2.4e-108:550:96//AC004895
R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6
. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a
beta-glucoronidase LIKE pseudogene. Contains a membrane protein LIKE ps
eudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudo
gene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences)
and a CA repeat polymorphism, complete sequence.//1.8e-103:552:93//AL02
1368
R-PLACE1007105//Mus musculus muskelin mRNA, complete cds.//2.7e-32:379:7
3//U72194
R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic
sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.14:422:57//AC00
4688
R-PLACE1007112//Cynips cornifex cytb gene.//0.020:427:58//AJ228479
R-PLACE1007132//Homo sapiens full length insert cDNA YH77E09.//5.7e-107:
535:96//AF074987
R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 u
nordered pieces.//0.36:408:58//AC005050
R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA.//0.99:6
3:73//AF009283
R-PLACE1007226
R-PLACE1007238
R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-
II, hS-II-T1, complete cds.//2.0e-91:534:89//D50495
R-PLACE1007242//CITBI-E1-2512M9.TF CITBI-E1 Homo sapiens genomic clone 2

512M9, genomic survey sequence.//1.3e-05:117:76//AQ279454
R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA
./0.21:284:58//U02970
R-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//6.9e-113:607:93/
/Y15908
R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394_K_10, complet
e sequence.//4.4e-10:135:74//AC006080
R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 g
ene, complete sequence.//1.7e-36:435:72//AF069291
R-PLACE1007282//B.garinii (strain TIs1) p83/100 gene (partial).//0.95:18
3:60//X81533
R-PLACE1007286//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-1
1-13L8, genomic survey sequence.//6.1e-55:519:76//B75158
R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Co
ntains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes.
Contains ESTs and STSS and a CpG island.//0.75:180:62//Z97195
R-PLACE1007317//Drosophila dasyncemia 16S ribosomal RNA gene, mitochondr
ial gene for mitochondrial RNA, partial sequence.//0.59:236:59//U94253
R-PLACE1007342
R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mR
NA, complete cds.//3.7e-65:367:91//AF096870
R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 geno
mic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:6
2//AC005507
R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomi
c sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC
004709
R-PLACE1007386//Reclinomonas americana mitochondrial DNA, complete genom
e.//0.0012:403:58//AF007261

R-PLACE1007402//HS_2055_A2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=6 Row=G, genomic survey sequence.//0.0046:88:79//AQ234824

R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771

R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594

R-PLACE1007450//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304

R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.6e-59:389:82//AC004081

R-PLACE1007460

R-PLACE1007478//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.0e-08:335:60//AC004241

R-PLACE1007484

R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//2.5e-05:421:61//AF072373

R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence.//2.3e-09:577:57//AL034559

R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.2e-79:387:96//AC004231

R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//3.4e-09:148:73//AC003682

R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//4.7e-38:297:82//AC004381

R-PLACE1007544

R-PLACE1007547//Human laminin alpha 4 chain (LAMA4*-1) mRNA, complete cds.//4.0e-17:108:97//U77706

R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence.//2.2e-45:390:77//AC002465

R-PLACE1007583//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 545L17, WORKING DRAFT SEQUENCE.//1.0e-56:302:95//AL031665

R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence.//1.5e-102:554:93//AF038179

R-PLACE1007618

R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence.//1.4e-103:537:94//AF038176

R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.3e-76:289:94//AC005840

R-PLACE1007645//Homo sapiens full length insert cDNA clone ZD76G10.//0.0080:96:77//AF086408

R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//1.1e-82:412:97//AQ022149

R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0041:470:57//AE001367

R-PLACE1007688

R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence.//1.3e-22:162:91//AC002044

R-PLACE1007697

R-PLACE1007705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//4.4e-121:624:95//AL031662

R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.8e-73:374:96//AF061243

R-PLACE1007725//Caenorhabditis elegans cosmid F38A5.//0.070:186:60//U708

R-PLACE1007729//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3' LTR./ /3.8e-53:415:81//U60269

R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2 .1e-92:556:89//AB014585

R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence.//4.0e-43:30 2:77//AF015169

R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence.//1.0e-0 6:533:59//AL034560

R-PLACE1007746//T.brucei mitochondrial maxicircle DNA encoding cytochrom e c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, co mplete cds.//0.28:386:58//M14820

R-PLACE1007791//D.discoideum gene for protein kinase.//0.17:263:60//Z379 81

R-PLACE1007807//Human DNA sequence from clone 87808 on chromosome Xq21.1 -21.33. Contains an EST, STSS, a GSS and genomic marker DXS472, complete sequence.//1.1e-72:324:88//AL031116

R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence.//2.2e-14:325:67//AF017104

R-PLACE1007829//Human BAC clone GS165I04 from 7q21, complete sequence.// 0.00052:455:61//AC002379

R-PLACE1007843//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.0050:447:57//X95275

R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr ome region), segment 3/15, WORKING DRAFT SEQUENCE.//2.2e-111:570:95//AP0 00010

R-PLACE1007852//HS_3028_B2_F04_MR CIT Approved Human Genomic Sperm Libra ry D Homo sapiens genomic clone Plate=3028 Col=8 Row=L, genomic survey s equence.//1.3e-12:209:71//AQ131021

R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//6
.6e-110:574:94//AB018309

R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome X
q25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome pr
oteins OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//1.6e-43:
551:70//AL022162

R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169),
complete sequence.//1.6e-22:222:78//AC005754

R-PLACE1007897//HS_3113_B2_E04_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey s
equence.//2.9e-72:381:95//AQ186905

R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487.//8.8e-88:460:95//AB007956

R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING
DRAFT SEQUENCE.//4.9e-23:172:78//AC003095

R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequen
ce.//1.7e-27:303:75//AC006157

R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, com
plete cds.//3.9e-102:513:95//AF084530

R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)
mRNA, partial cds.//2.2e-87:465:93//AF079529

R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA,
partial cds.//4.8e-72:556:81//U13262

R-PLACE1007990//E. tenella antigen LPMC61 mRNA, partial cds.//0.043:273:6
3//M30933

R-PLACE1008000//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346

R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4
unordered pieces.//9.0e-114:563:96//AC005628

R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:72//L31840

R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:66//AC005592

R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.082:292:59//AC006232

R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//AC005036

R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157

R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//1.9e-11:384:63//AC005919

R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955

R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06.//7.4e-47:320:86//D16939

R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849

R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748

R-PLACE1008198

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102

R-PLACE1008209//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//4.6e-16:250:71//AL034549

R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688

R-PLACE1008244//P.falciparum P.195 gene.//0.11:212:66//A04562

R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611
R-nnnnnnnnnnnnnnn
R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14
-15, complete sequence.//1.5e-05:104:76//AC005272
R-PLACE1008309//Human 'at'-rich region adjacent to alpha satellite DNA./
/0.70:138:63//M80308
R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q
25.1, complete sequence.//0.00061:150:68//AC005886
R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequ
ence.//4.8e-74:252:98//AC005176
R-PLACE1008331//Genomic sequence from Human 13, complete sequence.//1.0:
176:65//AC001226
R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA,
3' UTR.//2.5e-98:556:90//AF036145
R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C
Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey seq
uence.//1.2e-05:375:62//B36336
R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr
ome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP00
0011
R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471_L_13, complet
e sequence.//1.0e-46:282:82//AC005244
R-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417
R-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4
, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered
pieces.//0.18:379:58//AC004604
R-nnnnnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:
95//D86326

R-PLACE1008405//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//6.8e-22:3
28:71//U15177

R-PLACE1008424

R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of
hepatocellular colorectal and non-small cell lung cancer , segment 7/11.
//7.5e-101:505:96//AB020864

R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2
-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ra
s-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.
//1.2e-11:118:78//AL022576

R-PLACE1008437//H.sapiens genomic DNA (PAC 838L14) from chromosome 11, W
ORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335

R-PLACE1008455

R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus,
complete sequence.//1.2e-109:588:93//AC004526

R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone
A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696

R-PLACE1008488

R-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 34B21, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778

R-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C su
bunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555

R-PLACE1008532

R-PLACE1008533

R-PLACE1008568//HS_3218_B2_D08_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey
sequence.//0.0042:295:62//AQ214623

R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence./
/5.0e-26:254:66//AC003074

R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//4.0e-78:498:86//AC006120

R-nnnnnnnnnnnnnnn

R-PLACE1008626//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297

R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836

R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826

R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096

R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001

R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333

R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742

R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406

R-PLACE1008715//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147

R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP Homo sapiens genomic clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841

R-PLACE1008757//Homo sapiens 12q24.2 PAC RPCI4-765H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.99:211:61//AC00586

4

R-PLACE1008790//Rattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with

GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762
R-PLACE1008798//Homo sapiens full length insert cDNA clone YZ86C05.//7.7
e-58:285:100//AF086088
R-PLACE1008807//CIT-HSP-2366014.TR CIT-HSP Homo sapiens genomic clone 23
66014, genomic survey sequence.//3.5e-35:223:89//AQ079210
R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, compl
ete cds.//2.3e-97:499:95//AF030933
R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//9.7e-45:39
4:78//AF032668
R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DR
AFT SEQUENCE, 3 unordered pieces.//2.9e-28:207:87//AC004581
R-nnnnnnnnnnnnn//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 217
2B3, genomic survey sequence.//8.9e-30:166:97//B93289
R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequ
ence.//3.5e-76:404:95//AC005058
R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3
unordered pieces.//7.7e-37:585:67//AC004932
R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494_G_17, complete
sequence.//0.0022:409:60//AC005820
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.
2e-55:344:89//AB018308
R-PLACE1008925//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS **
* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860
R-PLACE1008934
R-PLACE1008941//Homo sapiens chromosome 17, clone hRPK.293_K_20, complet
e sequence.//9.8e-84:429:92//AC005495
R-PLACE1008947
R-PLACE1009020
R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23

Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117

R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.

1-22.3. Contains STSs, GSSs and a putative CpG island, complete sequence .//0.00010:297:58//AL031391

R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//2.9e-06:160:70//AC004707

R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.

3-25.1. Contains the last coding exon of the gene for P18 component of a minoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:339:66//AL023694

R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023

R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//0.00075:79:83//AJ005074

R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-13:212:73//AC004783

R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence./ /0.49:221:61//Z70206

R-PLACE1009099

R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-17:301:66//AC004025

R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140

R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//7.5e-06:426:58//Z98551

R-PLACE1009150//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRA

FT SEQUENCE.//2.3e-118:614:95//AJ011929
R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/
28, WORKING DRAFT SEQUENCE.//1.4e-107:584:93//AP000031
R-PLACE1009158//Homo sapiens full length insert cDNA clone YP10D03.//1.9
e-105:539:95//AF085876
R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180_P_8, complet
e sequence.//2.8e-44:360:71//AC005972
R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046
R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complet
e sequence.//2.1e-17:140:81//AC004925
R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6
q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein
Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs,
complete sequence.//1.9e-46:572:69//Z84480
R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC
004070
R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:
487:58//AL034560
R-PLACE1009200//H.sapiens mRNA for sortilin.//1.0e-31:195:92//X98248
R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531
) , complete sequence.//1.8e-75:364:85//AC005392
R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory elemen
t binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U2281
8
R-PLACE1009308
R-PLACE1009319//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Canc
er Institute Human PAC Library) complete sequence.//0.00010:132:75//AC00
4801
R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346_K_10, complet

e sequence.//3.3e-87:576:85//AC006120

R-PLACE1009335//*Borrelia burgdorferi* (section 62 of 70) of the complete genome.//0.32:315:60//AE001176

R-PLACE1009338//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140

R-PLACE1009368//*Homo sapiens* PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:61//AC004989

R-PLACE1009375//*D. yakuba* mitochondrial DNA for origin of replication, small ribosomal RNA, transfer RNAs tRNA-fMet, tRNA-Gln, tRNA-Ile and tRNA-Val.//1.1e-08:444:60//X05915

R-PLACE1009388

R-PLACE1009398//*Homo sapiens* BAC clone GS011E15 from 5q31, complete sequence.//0.065:279:61//AC002427

R-nnnnnnnnnnnnn//*Homo sapiens* clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038

R-PLACE1009410//*Homo sapiens* chromosome 17, clone hRPK.142_H_19, complete sequence.//9.8e-112:561:96//AC005919

R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120

R-PLACE1009443//*Homo sapiens* nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//AF064598

R-PLACE1009444//*Homo sapiens* phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151

R-PLACE1009459

R-PLACE1009476//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531

R-PLACE1009477//Homo sapiens, clone hRPK.15_A_1, complete sequence.//3.4e-46:284:91//AC006213

R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:92//U91321

R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22 q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSS and GSSs, complete sequence.//0.74:301:61//Z94160

R-PLACE1009539//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427

R-PLACE1009542//CIT-HSP-2166P10.TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614

R-PLACE1009571//RPCI11-61J16.TK RPCI11 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ202146

R-PLACE1009581

R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006

R-PLACE1009596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051

R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230

R-PLACE1009613//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-08:434:59//AL010266

R-PLACE1009621//Sequence 50 from patent US 5691147.//1.5e-20:235:73//I76222

R-PLACE1009622//CIT-HSP-2023D13.TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey sequence.//0.72:176:62//B81271

R-PLACE1009637//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276

R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project).//0.013:521:58//AL021811

R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159

R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534

R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011

R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109

R-PLACE1009731//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024

R-PLACE1009794

R-nnnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//7.5e-88:191:96//AL030996

R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6 q21. Contains an unknown gene, ESTs and STSS, complete sequence.//8.7e-19:226:69//Z98172

R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence.//2.1e-29:230:76//AG002672

R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:61//AC004945

R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//5.3e-91:577:88//AC006116

R-nnnnnnnnnnnnn

R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//4.7e-81:385:84//M63005

R-PLACE1009924//HS_3151_B1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412

R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence.//0.00010:159:68//B51673

R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308

R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483

R-PLACE1009971//Homo sapiens full length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247

R-PLACE1009992

R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:305:61//AE001367

R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10 q25.2-10q25.3, complete sequence.//1.8e-43:462:76//AC005874

R-PLACE1010023//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513

R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4e-115:581:96//AL031775

R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9e-05:136:74//X84692

R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey sequence.//2.6e-60:324:94//AQ042094

R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds./4.6e-87:543:88//AF065482

R-PLACE1010076//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0473M13; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.3e-08:489:58//AC005699

R-PLACE1010083

R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.//0.14:400:59//B10583

R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//X64411

R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556

R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.//4.0e-09:510:59//AE001374

R-PLACE1010106//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304

R-PLACE1010134

R-PLACE1010148//HS_3128_A1_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey sequence.//0.17:281:61//AQ140790

R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//3.1e-45:351:81//D38417

R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.6e-06:207:66//AC004928

R-PLACE1010194//HS_2232_B1_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey sequence.//2.4e-08:134:74//AQ185425

R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.2-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//0.00035:383:61//AL031585

R-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377

R-PLACE1010261

R-PLACE1010270//H.sapiens CpG island DNA genomic MseI fragment, clone 85a6, reverse read cpg85a6.rt1a.//0.068:171:63//Z63482

R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280

R-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464

R-PLACE1010321

R-PLACE1010324//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS ** * from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149

R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IG LC Region, complete sequence.//7.9e-35:328:79//AC000024

R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21

unordered pieces.//1.3e-31:418:66//AC004971

R-PLACE1010362

R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098

R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//1.4e-105:543:95//AC004675

R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137

R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927

R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081

R-PLACE1010492//HS_3169_B2_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892

R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082

R-nnnnnnnnnnnnnnn

R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929

R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein var1.//1.7e-05:271:65//X02893

R-PLACE1010580

R-PLACE1010599

R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465

R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//AF096370.

R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete sequence
./8.2e-34:322:79//AF053356

R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21
unordered pieces./2.3e-97:515:94//AC004846

R-PLACE1010629//HS_3003_A2_C08_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey
sequence./5.6e-60:321:95//AQ130493

R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of
the complete sequence./0.051:372:59//AE001382

R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds./2.
6e-92:497:93//AB011102

R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 20
08K15, genomic survey sequence./5.7e-27:160:95//B57089

R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence./
9.4e-09:151:73//Z81467

R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 231
4C3, genomic survey sequence./1.3e-90:459:96//AQ028536

R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-
Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene e
ncoding mitochondrial protein, complete cds./5.3e-08:478:58//U49822

R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mR
NA, partial cds./3.8e-55:300:95//AF092564

R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.
1-21.33. Contains GSSs, complete sequence./3.4e-89:507:90//Z95400

R-PLACE1010743

R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294_J_22, complet
e sequence./3.0e-103:511:97//AC005921

R-PLACE1010771

R-PLACE1010786

R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//1.8e-43:545:71//AC005682

R-PLACE1010802//Phoebis agarithe large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//1.9e-09:492:59//AF044862

R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence.//0.041:415:59//AC002524

R-PLACE1010833

R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512:55//AC004153

R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 11/11.//4.9e-85:507:90//AB020868

R-PLACE1010870//RPCI11-59K21.TK RPCI11 Homo sapiens genomic clone R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501:96//AB011182

R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489

R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409:59//AC005505

R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07:180:71//AB018488

R-PLACE1010916//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL034557

R-PLACE1010917

R-PLACE1010925//HS_2027_B2_B09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence.//1.6e-46:404:77//AQ247031

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402:89//AB011126

R-nnnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds.//1.9e-80:441:93//AF064243

R-PLACE1010944

R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533

R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518:74//AC005077

R-PLACE1010960//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//0.022:292:63//AL033522

R-PLACE1010965//Human mariner1 transposase gene, complete consensus sequence.//1.0e-64:444:84//U52077

R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.59:345:61//AJ235272

R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242

R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153

R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483

R-PLACE1011056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985

R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896

R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complet

e sequence.//0.12:489:59//AC005509

R-PLACE1011109//Homo sapiens chromosome Y, clone 486, 0, 2, complete sequence.//8.4e-43:427:76//AC002531

R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-14).//1.7e-29:179:94//Y16709

R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//B44006

R-PLACE1011143//H.sapiens CpG island DNA genomic MseI fragment, clone 127a4, forward read cpg127a4.ft1a.//1.0:127:67//Z56550

R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333

R-PLACE1011165//Human Cosmid g5129s232 from 7q31.3, complete sequence.//0.47:355:58//AC003968

R-PLACE1011185//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-26:403:70//AC004820

R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908

R-PLACE1011219//HS_3036_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587

R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000659

R-PLACE1011229//HS_3002_B1_E10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-31:317:74//AQ303626

R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.2e-109:571:94//AC005014

R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.00027:337:61//M97514

R-PLACE1011291

R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887

R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661

R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.0e-10:511:59//AE001398

R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344

R-PLACE1011340//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530

R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310

R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140

R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102

R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013

R-PLACE1011465

R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//7.9e-103:515:96//AB018255

R-PLACE1011492//A-837A4.TP CIT978SK Homo sapiens genomic clone A-837A4, genomic survey sequence.//6.5e-37:234:82//B14085

R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171_I_10, complete sequence.//0.99:267:60//AC004687

R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-16:591:96//AC004968

R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688

R-PLACE1011567//Plasmodium falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551

R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973

R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477

R-PLACE1011635//C.pasteurianum pf1 gene and act gene.//0.71:288:60//X93463

R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205

R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620

R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535

R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477

R-PLACE1011664//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905

R-PLACE1011675//CIT-HSP-2370M16.TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283

R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776

R-PLACE1011719//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Can

cer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806

R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526

R-PLACE1011729//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9; WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345

R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089

R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//1.9e-35:538:68//AC002383

R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782

R-PLACE1011783//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090

R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321

R-PLACE1011874//Homo Sapiens Chromosome X clone bWXd312, complete sequence.//2.1e-100:511:95//AC004478

R-PLACE1011875

R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193

R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398

R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090

R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds./

/7.0e-98:546:92//AF059617

R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 22
94L24, genomic survey sequence.//0.31:131:63//AQ006352

R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete s
equence.//2.5e-08:393:63//AC002994

R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone
: MDJ14, complete sequence.//9.6e-09:463:62//AB016889

R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1
-2H4.//2.7e-39:294:82//U44738

R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.
5e-104:540:95//AB018256

R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//
4.9e-10:439:63//AC004000

R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene,
intron 3.//1.0:151:66//L78722

R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence./
/1.5e-103:524:95//AF091080

R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequ
ence.//0.94:372:57//AC005191

R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162_E_12, complet
e sequence.//3.0e-55:299:86//AC006236

R-PLACE2000021//CIT-HSP-2343C18.TR CIT-HSP Homo sapiens genomic clone 23
43C18, genomic survey sequence.//4.5e-54:295:94//AQ058140

R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit
(P1 form).//6.5e-38:298:82//X69907

R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4
unordered pieces.//5.3e-34:200:79//AC005628

R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequ
ence.//1.8e-49:274:89//AC003083

R-PLACE2000047//CIT-HSP-2373C2.TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey sequence.//1.8e-48:389:79//AQ112243

R-PLACE2000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.//0.0027:95:76//AL022315

R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429:72//AB011147

R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.9e-40:310:84//AC004832

R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550:95//AF027219

R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-106:553:95//AC005910

R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-38:285:84//AL031730

R-PLACE2000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//4.3e-113:559:97//AL031848

R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricel light chain, exon 1.//0.00041:347:61//X16325

R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165:63//U63067

R-PLACE2000132

R-PLACE2000136//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence.//0.0032:310:61//AL008974

R-PLACE2000140//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//1.1e-111:566:96//AL020995

R-PLACE2000164

R-PLACE2000170//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4

, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.9e-40:390:76//AC005598

R-PLACE2000172

R-PLACE2000176

R-PLACE2000187//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268H5, WORKING DRAFT SEQUENCE.//8.7e-45:298:87//AL008718

R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:495:92//L02897

R-PLACE2000223

R-PLACE2000235//HS_3159_B1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3159 Col=11 Row=D, genomic survey sequence.//1.8e-88:454:96//AQ179271

R-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//9.1e-41:282:86//AC005902

R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome X p11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//8.3e-35:305:80//Z97181

R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325:67//AC002394

R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//AC003043

R-PLACE2000305//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//1.2e-43:295:85//Z93015

R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tpx3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-05:284:65//Z92542

R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.5e-26:334:70//AC006147

R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGFII, TH, NAP2 genes.//4.0e-05:254:64//AL021880

R-PLACE2000347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE.//1.6e-82:504:88//AL022147

R-PLACE2000359//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 40E16, WORKING DRAFT SEQUENCE.//2.0e-36:314:80//AL031963

R-PLACE2000366//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//2.0e-48:389:80//AL031291

R-PLACE2000371

R-PLACE2000373//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 324M8, WORKING DRAFT SEQUENCE.//0.61:231:61//AL008734

R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence.//3.5e-11:287:67//AC004917

R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//6.8e-108:553:96//AL031432

R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.9e-26:326:73//AC005059

R-PLACE2000399

R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//6.5e-84:434:96//AC005216

R-PLACE2000411//P.clarkii mRNA; repeat region (ID 2R).//0.47:104:70//Z54273

R-PLACE2000419

R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.9e-40:447:74//AF003528

R-PLACE2000427

R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence.//3.5e-40:286:85//AC000379

R-PLACE2000435

R-PLACE2000438//Homo sapiens full length insert cDNA clone ZE04D01.//2.2e-107:523:98//AF086521

R-PLACE2000450

4.1e-42:328:79//AG006257

R-PLACE2000455

R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.1e-116:570:97//AC005740

R-PLACE2000465//Human BAC clone RG191D16, complete sequence.//6.3e-37:408:75//AC002460

R-PLACE2000477//M.musculus tex264 mRNA (3' region).//7.5e-06:117:76//X80427

R-PLACE3000004

R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSS and a CpG island.//5.8e-34:308:78//Z82976

R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-36:273:87//Y17267

R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//2.3e-10:181:71//AC004648

R-PLACE3000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495:74//AL022156

R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion Region, complete sequence.//3.4e-39:283:85//AC000026

R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//9.2e-23:171:76//AC005200

R-PLACE3000136//U.arctos microsatellite DNA, clone UarMU23.//0.00052:171

:65//Y09645

R-PLACE3000142//HS_3037_B2_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence.//0.88:121:66//AQ097023

R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:472:66//AB001735

R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//3.5e-11:176:73//Z49237

R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//6.9e-106:549:94//AC005277

R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//7.0e-38:545:70//AC002383

R-PLACE3000157

R-PLACE3000158//, complete sequence.//1.4e-33:283:81//AC005500

R-PLACE3000160

R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//5.2e-43:229:85//AC006130

R-PLACE3000194

R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//7.2e-61:394:89//AC005291

R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes; complete cds, and Xq28lu2 gene.//0.23:309:57//U52112

R-PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384 B14, genomic survey sequence.//1.1e-15:156:81//B54637

R-PLACE3000208//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 591N18, WORKING DRAFT SEQUENCE.//1.3e-16:139:87//AL031594
R-PLACE3000218//HS_3185_B1_B01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=1 Row=D, genomic survey sequence.//3.5e-07:120:75//AQ155720
R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//2.4e-44:363:80//AC004167
R-PLACE3000226//Caenorhabditis elegans cosmid M01G5.//0.88:95:77//AF078786
R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.3e-69:536:81//U95626
R-PLACE3000242//Sequence 1 from patent US 5599918.//3.2e-62:546:78//I35489
R-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.7e-45:404:75//X80169
R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds.//7.5e-28:174:94//AB002307
R-PLACE3000271//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//3.9e-54:492:77//AL034379
R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//5.4e-12:176:69//AC004081
R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//5.7e-114:555:97//AC005328
R-PLACE3000310//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467L1, WORKING DRAFT SEQUENCE.//6.2e-51:314:84//Z98884
R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds.//2.5e-44:289:90//U93037
R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3.//5.9e-20:153:88//M21006

R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-43:230:84//AC005480

R-PLACE3000339

R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-111:550:97//AC006055

R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSS and GSSs, complete sequence.//1.5e-44:314:78//AL022323

R-PLACE3000352//HS_3095_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=17 Row=J, genomic survey sequence.//8.5e-73:356:99//AQ123142

R-PLACE3000353//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS ** * from clone Y22F5, WORKING DRAFT SEQUENCE.//0.21:194:63//Z99712

R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7.//0.26:360:60//AJ002197

R-PLACE3000363

R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence.//4.6e-52:487:76//AC002465

R-PLACE3000373//HS_3202_B1_G05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3202 Col=9 Row=N, genomic survey sequence.//2.4e-75:437:90//AQ252699

R-PLACE3000388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//6.4e-61:515:81//AL008722

R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00098:444:60//AC005231

R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506

R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25
unordered pieces.//8.0e-47:223:81//AC006023

R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003

R-PLACE3000405//Homo sapiens chromosome 7qtelo BAC F6, complete sequence
.//2.4e-44:466:74//AF104455

R-PLACE3000406//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718

R-PLACE3000413

R-PLACE3000416//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 157
7, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612

R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-2
2.3. Contains ribosomal protein L29 pseudogene, ESTs and STSS.//1.1e-41:
366:78//AL008627

R-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284

R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92//U43899

R-PLACE3000477

R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to
heyman nephritis antigen gp330.//6.6e-17:344:68//Z11995

R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.
7e-83:433:95//AB018352

R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosmid
Homo sapiens genomic clone cSRL-51C5, genomic survey sequence.//0.54:
116:66//B04984

R-PLACE4000049//Human BAC clone GS165I04 from 7q21, complete sequence.//
0.29:313:59//AC002379

R-PLACE4000052//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***

from MAL4P1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557

R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence
 .//0.98:246:61//AF053356

R-PLACE4000089//RPCI11-15I1.TVB RPCI-11 Homo sapiens genomic clone RPCI-
 11-15I1, genomic survey sequence.//3.2e-07:284:60//B82414

R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic
 sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//
 AC005506

R-PLACE4000100

R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3
 e-100:419:91//AF055010

R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete
 sequence.//9.6e-45:284:90//AC003007

R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0500.//1.6e-19:118:100//AB007969

R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequen
 ce.//8.9e-17:208:73//AC005034

R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome
 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and
 slime mold hypothetical genes, and a gene coding for an aldehyde dehydr
 ogenase family protein. Contains ESTs, STSS and GSSs, complete sequence.
 //3.7e-43:281:90//AL021939

R-PLACE4000192

R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25
 unordered pieces.//5.4e-44:280:82//AC005631

R-PLACE4000233//Homo sapiens full length insert cDNA YH59G06.//1.8e-79:4
 14:97//AF074981

R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156_L_14, complet
 e sequence.//5.7e-59:558:76//AC005821

R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381

R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.5e-39:311:83//AC005920

R-PLACE4000261//H.sapiens BF1P-glH03np gene for immunoglobulin heavy chain in variable region.//0.33:197:61//Z80410

R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//1.4e-31:327:68//AC005510

R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.3e-32:345:74//D87675

R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003339

R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 C contains STS, GSS, complete sequence.//8.2e-41:295:85//Z99495

R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.3e-32:404:75//U73640

R-PLACE4000326

R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//0.32:135:68//AC005587

R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:67//Y07829

R-PLACE4000369//HS_3181_A1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222

R-PLACE4000379//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//1.7e-05:160:65//AL022312

R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-47:351:81//AC004913

R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13.

Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence
./8.5e-88:541:88//AL034377

R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ23
9b22, WORKING DRAFT SEQUENCE, 17 unordered pieces./2.7e-17:143:83//AC00
0406

R-PLACE4000411

R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4
unordered pieces./0.028:91:78//AC005628

R-PLACE4000465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 30A23, WORKING DRAFT SEQUENCE./1.6e-43:532:71//AL022156

R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of
the complete sequence./4.1e-06:357:61//AE001427

R-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Can
cer Institute Human PAC Library) complete sequence./2.7e-37:416:74//AC0
05865

R-PLACE4000522

R-PLACE4000548//Homo sapiens 12p13.3 PAC RPCI5-1096D14 (Roswell Park Can
cer Institute Human PAC Library) complete sequence./0.0020:383:60//AC00
5342

R-PLACE4000558//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cance
r Institute Human BAC library) complete sequence./2.9e-44:465:75//AC002
996

R-THYR01000026//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 37E16, WORKING DRAFT SEQUENCE./2.2e-43:354:82//Z83844

R-THYR01000034//Plasmodium falciparum chromosome 2, section 59 of 73 of
the complete sequence./0.022:327:60//AE001422

R-THYR01000035//HS_3018_B2_F10_T7 CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey
sequence./2.3e-36:228:91//AQ092318

R-THYRO1000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157

R-THYRO1000070//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.//1.1e-44:284:89//U14573

R-THYRO1000072//***ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:83//U14567

R-THYRO1000085

R-THYRO1000092//Homo sapiens chromosome 7qtelo BAC F6, complete sequence.//3.3e-36:301:78//AF104455

R-THYRO1000107//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 125I3, WORKING DRAFT SEQUENCE.//1.4e-35:282:82//AL033528

R-THYRO1000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//4.0e-32:351:65//AC002300

R-THYRO1000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//6.6e-77:507:85//U91318

R-THYRO1000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.66:334:59//AC005840

R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//2.3e-88:449:96//AF087142

R-THYRO1000132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//1.1e-40:298:84//Z95114

R-THYRO1000156//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//3.4e-37:425:73//AC005703

R-THYRO1000163//RPCI11-1B20.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1B20, genomic survey sequence.//8.4e-38:276:84//B63536

R-THYRO1000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island.//1.1e-70:553:81//Z83841

R-THYRO1000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c

lone 41018, WORKING DRAFT SEQUENCE.//6.7e-41:345:81//AL031732
R-THYRO1000187//Human thymopoietin (TMPO) gene, partial exon 6, complete
exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.3e-43
:356:80//U18271
R-THYRO1000190//Homo sapiens chromosome 17, clone HRPC843B9, complete se
quence.//2.6e-40:386:77//AC004139
R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//1.
1e-108:535:97//AJ005698
R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1
.4e-113:559:97//AB014552
R-THYRO1000206//Rat PMSG-induced ovarian mRNA, 3' sequence, N4.//4.0e-43:
318:86//D84482
R-THYRO1000221//Human DNA from overlapping chromosome 19 cosmids R31396,
F25451, and R31076 containing COX6B and UPKA, genomic sequence, complet
e sequence.//2.7e-44:452:76//AC002115
R-THYRO1000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal lo
cation, complete sequence.//4.8e-58:447:81//AC000039
R-THYRO1000242
R-THYRO1000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome
6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternati
vely spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MA
PK p38beta LIKE protein. Contains ESTs, STSS and two predicted CpG islan
ds, complete sequence.//3.4e-56:300:84//Z95152
R-THYRO1000270
R-THYRO1000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 531H16, WORKING DRAFT SEQUENCE.//4.8e-113:584:96//AL031664
R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//1.1e-98:
566:91//AB016068
R-THYRO1000320//HS_2033_B1_A07_T7 CIT Approved Human Genomic Sperm Libra

ry D Homo sapiens genomic clone Plate=2033 Col=13 Row=B, genomic survey
sequence.//0.97:211:63//AQ233366

R-THYRO1000327//Sequence 1 from patent US 5541298.//2.8e-52:289:93//I240
58

R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//1.
1e-111:559:96//AB018333

R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds
.//4.6e-47:317:87//U29091

R-THYRO1000368//HS_3049_A1_E12_MF CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3049 Col=23 Row=I, genomic survey
sequence.//7.0e-11:111:83//AQ126777

R-nnnnnnnnnnnnnnn

R-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete
sequence.//2.4e-101:545:93//AC006019

R-THYRO1000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 cont
aining uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1
.6e-46:233:88//AC006078

R-THYRO1000395//Mouse MIPP mRNA for a placenta-expressed gene.//2.3e-57:
395:85//X58523

R-THYRO1000401

3.3e-111:546:97//AF051907

R-THYRO1000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6
unordered pieces.//2.7e-44:289:89//AC005231

R-THYRO1000452//Homo sapiens chromosome 17, clone hRPK.243_K_12, complet
e sequence.//6.7e-27:222:82//AC005668

R-THYRO1000471//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 102D24, WORKING DRAFT SEQUENCE.//2.4e-36:369:76//AL021391

R-THYRO1000484//Homo sapiens clone DJ1099N07, complete sequence.//1.6e-4
3:288:81//AC004962

R-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.6e-95:512:94//AC005740

R-THYRO1000501//HS_2208_A1_G11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence.//0.0063:189:63//AQ091586

R-THYRO1000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987

R-THYRO1000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//AC004798

R-THYRO1000558

R-THYRO1000569

R-THYRO1000570//Homo sapiens full length insert cDNA clone ZD76G10.//4.3e-41:209:100//AF086408

R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//8.2e-107:533:97//AF075587

R-THYRO1000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial cds.//0.36:170:67//AF006072

R-THYRO1000602//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.2e-53:289:92//D87675

R-THYRO1000605

R-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//1.3e-31:261:82//AC005546

R-THYRO1000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-06:249:63//AL022323

R-THYRO1000641//P.falciparum glutamic acid-rich protein gnen, complete cds.//3.1e-08:244:68//J03998

R-THYRO1000658//***ALU WARNING: Human Alu-Sp subfamily consensus sequenc

e.//3.9e-49:282:93//U14572

R-nnnnnnnnnnnnn

R-THYRO1000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005

R-THYRO1000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//1.2e-06:227:64//AC004069

R-THYRO1000684

R-THYRO1000699

R-THYRO1000712

R-THYRO1000734//Human BAC clone RG191D16, complete sequence.//3.7e-14:468:64//AC002460

R-THYRO1000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533

R-THYRO1000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//I25660

R-THYRO1000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558

R-THYRO1000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey sequence.//1.2e-81:391:99//AQ038226

R-THYRO1000787//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//9.4e-07:494:58//AC004617

R-THYRO1000793

R-THYRO1000796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19, WORKING DRAFT SEQUENCE.//1.7e-42:379:79//Z93014

R-THYRO1000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENCE, 18 unordered pieces.//4.7e-40:362:76//AC002555

R-THYRO1000815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//4.0e-58:295:92//Z82199

R-THYRO1000829//Sequence 7 from patent US 5716622.//0.97:362:61//I87788
R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 fr
om the Prader-Willi/Angelman Syndrome region, complete sequence.//3.3e-5
7:522:76//AC004738
R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKIN
G DRAFT SEQUENCE, 9 unordered pieces.//4.2e-17:291:69//AC005849
R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12
.2-12.3. Contains GSSs, complete sequence.//1.1e-41:419:75//AL031592
R-THYRO1000865//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 1125A11, WORKING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549
R-THYRO1000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 380F5, WORKING DRAFT SEQUENCE.//3.7e-111:569:96//AL031719
R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6
unordered pieces.//1.0e-97:554:92//AC006015
R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)
mRNA, partial cds.//9.6e-109:566:94//AF079529
R-THYRO1000934//Homo sapiens full length insert cDNA clone ZD69A10.//1.6
e-104:539:95//AF086378
R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAF
T SEQUENCE, 29 unordered pieces.//8.9e-61:479:81//AC004229
R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA.//
5.3e-16:116:93//M28639
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, co
mplete cds.//3.2e-59:321:95//AF047440
R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequ
ence.//1.9e-44:396:79//AC006126
R-THYRO1000983//Homo sapiens chromosome 17, clone hRPK.271_K_11, complet
e sequence.//0.99:71:78//AC005562
R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 cont

aining uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6
.7e-42:320:84//AC006078

R-THYR01000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome X
p11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z8
4466

R-THYR01001003//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey s
equence.//2.5e-39:310:83//AQ253727

R-THYR01001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome X
p11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z8
4466

R-THYR01001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 20
07J14, genomic survey sequence.//5.1e-26:143:100//B56677

R-THYR01001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2
386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882

R-THYR01001093

R-THYR01001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complet
e sequence.//0.47:102:73//AC005070

R-THYR01001120

R-THYR01001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//
8.9e-81:429:94//AJ006417

R-THYR01001133//CIT-HSP-2381I10.TR CIT-HSP Homo sapiens genomic clone 23
81I10, genomic survey sequence.//4.7e-12:237:67//AQ111077

R-THYR01001134

R-THYR01001142//H.sapiens CpG island DNA genomic MseI fragment, clone 81
d1, reverse read cpg81d1.rtl1a.//0.95:214:60//Z56037

R-THYR01001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cos
mid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6
e-26:262:77//B04145

R-THYRO1001177

R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973

R-THYRO1001204

R-THYRO1001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581

R-THYRO1001262//Homo sapiens, clone hRPK.16_A_1, complete sequence.//8.7e-53:442:79//AC006227

R-THYRO1001271//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630

R-THYRO1001290

R-THYRO1001313//H.sapiens CpG island DNA genomic MseI fragment, clone 19 5h3, forward read cp9195h3.ft1b.//0.046:126:66//Z57783

R-THYRO1001320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207

R-THYRO1001321//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558

R-nnnnnnnnnnnnnnn

R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288

R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92//B05884

R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10 q25, complete sequence.//1.8e-109:584:94//AC005660

R-THYRO1001374

R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953

R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence

e.//8.7e-38:307:82//AC002377

R-THYRO1001405

R-THYRO1001406//RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297

R-THYRO1001411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123

R-THYRO1001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553

R-THYRO1001434//Microcentus caryae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877

R-THYRO1001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578

R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-99:517:95//AC006001

R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085

R-THYRO1001534//HS_2242_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326

R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 C contains GSSs, complete sequence.//0.42:323:60//AL023876

R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077

R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCI5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868

R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic

sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308

R-THYR01001573//M.avium rpsL gene.//0.98:131:66//X80120

R-THYR01001584//A.longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653

R-THYR01001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808

R-THYR01001602//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//4.4e-13:320:67//AC005919

R-THYR01001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249

R-THYR01001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190

R-THYR01001637//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671

R-THYR01001656//HS_2201_B2_A08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence.//0.096:162:63//AQ293168

R-THYR01001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954

R-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//AJ225089

R-THYR01001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426

R-THYR01001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072

R-THYR01001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011

R-THYR01001721//, complete sequence.//1.3e-101:571:92//AC005500

R-nnnnnnnnnnnnnnn

R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//1.1e-15:193:70//AC004777

R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244

R-THYRO1001772//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156

R-THYRO1001793

R-THYRO1001809//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728

R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//5.0e-41:245:87//AC005696

R-THYRO1001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence.//4.4e-12:419:61//AC005137

R-THYRO1001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence.//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Luman mRNA, complete cds.//1.3e-23:138:98//AF009368

R-Y79AA1000013

R-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027

R-Y79AA1000037//CIT-HSP-2334F3.TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673

R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203:63//D2107

9

R-Y79AA1000131//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0548N01; HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered

pieces.//7.0e-18:169:79//AC004795
R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474:98//AL031864
R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074
R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386:90//AC004854
R-Y79AA1000230//Cytauxzoon felis 18S ribosomal RNA.//1.0:167:62//L19080
R-Y79AA1000231//HS_3009_A1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=0, genomic survey sequence.//6.4e-52:348:88//AQ090225
R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558
R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047
R-Y79AA1000313//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540
R-Y79AA1000328
R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107
R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611
R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692
R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protei

n pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163
R-Y79AA1000368
R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI
-11-16B12, genomic survey sequence.//0.10:171:65//B88000
R-Y79AA1000410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097
R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozo
ite surface protein 5, merozoite surface protein 2, and adenylosuccinat
e lyase genes, complete cds.//0.071:474:57//AF033037
R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-8
6:221:90//AC005033
R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complet
e sequence.//2.1e-14:179:72//AC004057
R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4
unordered pieces.//4.5e-43:321:83//AC005282
R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequen
ce.//0.0012:275:59//AC006143
R-Y79AA1000540//Z.diploperennis repetitive DNA (clone ZEAR 260).//0.0017
:258:62//X53609
R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X1497
2
R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete seque
nce.//0.96:224:61//AC002325
R-Y79AA1000627//Homo sapiens full length insert cDNA ZA77G02.//6.3e-100:
533:94//AF075117
R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7,
genomic survey sequence.//4.6e-88:429:98//AQ268433
R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA
, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433

R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00034:520:55//AC005505

R-Y79AA1000794//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 989H11, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851

R-Y79AA1000800//M.musculus tex264 mRNA (3' region).//1.1e-06:104:78//X80427

R-nnnnnnnnnnnnn//CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605

R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//3.1e-26:423:68//U73642

R-Y79AA1000824//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832

R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//AF083344

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647

R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey sequence.//0.00019:253:65//AQ013111

R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253

R-Y79AA1000969

R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 235

0C4, genomic survey sequence.//3.3e-60:295:100//AQ061422
R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:34
8:76//U05823
R-Y79AA1001023
R-Y79AA1001041
R-Y79AA1001048
R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10;
complete sequence.//1.2e-60:537:78//AC004626
R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete seque
nce.//2.3e-41:405:77//AC005031
R-Y79AA1001077
R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Canc
er Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC00
4801
R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasm
id pSK639.//0.0072:309:63//U40259
R-Y79AA1001145//RPCI11-59N12.TK RPCI11 Homo sapiens genomic clone R-59N1
2, genomic survey sequence.//3.7e-07:256:64//AQ200068
R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndr
ome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP00001
2
R-Y79AA1001177//Human gene for Gi3 alpha protein, intron 7 through exon
9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69
//X54048
R-Y79AA1001185
R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Can
cer Institute Human BAC Library) complete sequence.//2.1e-32:277:81//AC0
05912
R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.9

8:325:59//U47924

R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone
: MAB16, complete sequence.//0.0034:378:59//AB018112

R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5
unordered pieces.//0.19:106:72//AC004988

R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequ
ence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)
).//3.4e-109:549:95//AJ005892

R-Y79AA1001281

R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y
17126

R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymeras
e pseudogene, partial cds.//0.0070:284:58//U45372

R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic sur
vey sequence.//0.11:125:70//AL025355

R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.070:209:6
5//X66594

R-Y79AA1001391//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745

R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, comp
lete sequence.//0.99:241:63//AC004221

R-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer
Institute Human PAC Library) complete sequence.//0.25:81:80//AC005924

R-Y79AA1001493

R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12
Contains ESTs and GSSs, complete sequence.//1.3e-35:207:95//AL034430

R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53
) , complete cds.//2.7e-44:285:81//D14336

R-nnnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.2

2-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574

R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151

R-Y79AA1001555

R-Y79AA1001585

R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722

R-Y79AA1001603//H.sapiens CpG island DNA genomic MseI fragment, clone 72 f8, forward read cpg72f8.ft1a.//3.3e-21:131:96//Z62766

R-Y79AA1001613

R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS119 2 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975

R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008

R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743

R-nnnnnnnnnnnnn//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792

R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178

R-Y79AA1001705

R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139

R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402

R-nnnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044

R-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//2.3e-90:
557:89//U74297

R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome
6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternati
vely spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MA
PK p38beta LIKE protein. Contains ESTs, STSS and two predicted CpG islan
ds, complete sequence.//2.1e-34:306:78//Z95152

R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369

R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clon
e: K23L20, complete sequence.//0.0089:527:58//AB016874

R-Y79AA1001874

R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X8965
0

R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-2
6.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related
, matrix associated, actin dependent regulator of chromatin, subfamily a
, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains
ESTs, STSS and GSSs, complete sequence.//1.0:138:68//AL022577

R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA./
/0.71:153:67//X04465

R-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from c
lone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319

R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 u
nordered pieces.//6.3e-49:377:81//AC005011

R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-3
2:174:99//L77612

R-Y79AA1002103//CIT-HSP-2328I21.TR CIT-HSP Homo sapiens genomic clone 23
28I21, genomic survey sequence.//1.9e-44:245:96//AQ044502

R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone

2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752
R-Y79AA1002125//RPCI11-15J6.TV RPCI-11 Homo sapiens genomic clone RPCI-1
1-15J6, genomic survey sequence.//8.5e-21:147:91//B75354
R-Y79AA1002139
R-Y79AA1002204
R-nnnnnnnnnnnnn//Human ankyrin G (ANK-3) mRNA, complete cds.//0.040:319:5
9//U13616
R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4)./
/0.99:106:65//X65415
R-Y79AA1002210
R-Y79AA1002211//H.sapiens NGAL gene.//1.0:311:59//X99133
R-Y79AA1002220//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***
from MAL4P1, WORKING DRAFT SEQUENCE.//5.9e-07:535:57//AL034557
R-Y79AA1002229
R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.
1e-117:564:98//AB014592
R-Y79AA1002246
R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-92:453:9
7//AB013384
R-Y79AA1002298//HS_3071_B2_E08_MR CIT Approved Human Genomic Sperm Libra
ry D Homo sapiens genomic clone Plate=3071 Col=16 Row=J, genomic survey
sequence.//1.9e-56:384:87//AQ171331
R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.
5e-108:403:99//AB014534
R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173I12 map 10
q25, complete sequence.//1.1e-07:368:61//AC005887
R-Y79AA1002351
R-Y79AA1002361//H.sapiens CpG island DNA genomic MseI fragment, clone 65
b9, reverse read cpg65b9.rt1a.//0.57:59:79//Z62206

R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//2.0e-98:385:99//AC005920

R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//5.4e-59:490:76//AC004662

R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//6.3e-08:103:80//AC004087

R-Y79AA1002431

R-nnnnnnnnnnnn//Mouse transcriptional control element.//0.064:84:71//M17284

R-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.6e-103:525:96//AC006116

R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//9.7e-38:302:83//AC006238

R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

【 0 8 2 7 】

相同性検索結果データ 4.

5' 末端クローン配列に対する Human Unigene 相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータの Title、

P 値: 比較配列の長さ (base): 相同性 (%),

トップヒットデータの Accession No. の順に // で区切って記載した。

なお、相同性のスコアの P 値が 1 より大であった場合はデータは示さない。

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069

F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:L40157

F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U836

68

F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078
 F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247
 F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HE
 LICASE PRP22 [*Saccharomyces cerevisiae*]//0.00019:192:65//Hs.7900:W22411
 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759
 F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910
 F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734
 F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p1
 10delta mRNA, complete cds//0.27:342:61//Hs.14207:U86453
 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8
 e-169:791:98//Hs.27197:AB018340
 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4
 e-37:243:88//Hs.2397:Z70200
 F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is nov
 el. [*H.sapiens*]//5.3e-80:383:98//Hs.135552:AI215187
 F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//
 2.1e-07:265:63//Hs.85313:AF071309
 F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079
 F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYP
 ROTIN [*H.sapiens*]//1.3e-18:111:96//Hs.163863:W28729
 F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802
 F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI240133
 F-HEMBA1000201//Human Inil mRNA, complete cds//6.5e-75:440:92//Hs.155626
 :U04847
 F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529
 F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//
 Hs.8136:U81984
 F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, co
 mplete cds//1.3e-05:311:64//Hs.81248:U63289

F-HEMBA1000231
 F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377
 F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703
 F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460
 F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562
 F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568
 F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186
 F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406
 F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664
 F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:AI206095
 F-HEMBA1000303
 F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946
 F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:AI124898
 F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965
 F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961
 F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.99189:X84712
 F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.020:334:59//Hs.23094:M19503
 F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548
 F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802
 F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087
 F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H74010
 F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433

:58//Hs.159899:AC004853
 F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878
 F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320
 F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712:95//Hs.22900:AC004520
 F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533
 F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351:70//Hs.138992:C14008
 F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915
 F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI079253
 F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:AI032875
 F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616:66//Hs.159897:AB007970
 F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034
 F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398
 F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893
 F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI032875
 F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590
 F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853
 F-HEMBA1000469
 F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//0.15:253:58//Hs.104640:AF000561
 F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539:56//Hs.82709:Z22551
 F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970
 F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155095:D13666

F-HEMBA1000505//Homo sapiens KE04p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093

F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646

F-HEMBA1000518

F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI281881

F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cdna CEE SB82F [C.elegans]//2.9e-16:132:84//Hs.155871:AA533783

F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//2.1e-25:192:87//Hs.22383:R51067

F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]//2.4e-57:288:97//Hs.116022:AA455706

F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080

F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809

F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389

F-HEMBA1000545//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:K00629

F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684

F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729

F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:AB018303

F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI338977

F-HEMBA1000568//EST//0.12:270:61//Hs.134833:AI091046

F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042

F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681
 F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy c
 hain [C.elegans] //7.7e-41:217:96//Hs.55084:AA479162
 F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e
 -44:228:97//Hs.155218:AJ007509
 F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens] //1.7
 e-27:463:65//Hs.13794:AA203241
 F-HEMBA1000594//Human clone 230971 defective mariner transposon Hsmar2 m
 RNA sequence//4.0e-68:574:79//Hs.159176:U92019
 F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI092535
 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7
 e-120:561:99//Hs.5003:AB007925
 F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68/
 /Hs.153563:AF011333
 F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.col
 i] //7.4e-22:166:84//Hs.26252:AA643235
 F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1
 e-138:639:99//Hs.60103:AB014590
 F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174
 F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582
 F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI123912
 F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-4
 7:366:79//Hs.96247:X95073
 F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878
 F-HEMBA1000686
 F-HEMBA1000702
 F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309
 F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850
 F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630

F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI281881
 F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491
 F-HEMBA1000747
 F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568
 F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716
 F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239
 F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803
 F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216
 F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300
 F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536
 F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542
 F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367
 F-HEMBA1000843
 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X
 69962
 F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572
 F-HEMBA1000867
 F-HEMBA1000869//ESTs//5.1e-33:166:77//Hs.141186:R99609
 F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237
 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047
 F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660
 F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154
 F-HEMBA1000910//Human DNA sequence from clone 1409 on chromosome Xp11.1-
 11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a
 alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6
 -Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. C
 ontains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z
 98046
 F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537

F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142

F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:AB011119

F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens] //9.4e-10:77:93//Hs.111445:H00596

F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens] //0.0039:54:92//Hs.58338:AA609476

F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199

F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens] //0.080:128:71//Hs.118972:AA761369

F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161

F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:A1127903

F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775

F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314

F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.3e-05:424:59//Hs.159564:AF061936

F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.127338:AB007961

F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132

F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895

F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835

F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.46468:U45984

F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529

F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:AB007937

F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572

F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238

F-HEMBA1001022

F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.159897:AB007970

F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142

F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515

F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881

F-HEMBA1001052//EST//0.94:149:67//Hs.131216:AI017971

F-HEMBA1001059//N-ACETYLGALACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159479:U06088

F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813

F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420

F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//Hs.147802:R71297

F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172

F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248

F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284

F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017

F-HEMBA1001099

F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4e-6

1:341:85//Hs.5247:AF029750
 F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497
 F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940
 F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917
 F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747
 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341
 F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582
 F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457
 F-HEMBA1001174//ESTs//1.4e-63:363:92//Hs.132798:AA922226
 F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.mu sculus] //5.0e-54:555:71//Hs.55165:AA573499
 F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463
 F-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717
 F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694
 F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748
 F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058
 F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046
 F-HEMBA1001265
 F-HEMBA1001281
 F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155
 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:AC004131

F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119
534:AJ224741

F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs
.155464:AF088219

F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53
:272:97//Hs.154563:AI129590

F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.
norvegicus]//2.6e-66:241:99//Hs.120847:AA731201

F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873

F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.2
3:562:58//Hs.22039:AB018301

F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2
.5e-31:165:99//Hs.152213:L20861

F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN
FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68/
/Hs.108734:AI073427

F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013

F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)
mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358

F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794

F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074

F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156

F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353

F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sap
iens]//1.0e-132:643:97//Hs.124217:AA020848

F-HEMBA1001388

F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660

F-HEMBA1001398

F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117
 F-HEMBA1001407//ESTs//0.53:390:57//Hs.150447:AI017798
 F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108
 F-HEMBA1001413
 F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605
 F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040
 F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726
 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducibl
 e), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053
 F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031
 F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.mu
 sculus]//6.8e-47:550:71//Hs.55165:AA573499
 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIP1) mRNA, com
 plete cds//0.82:312:58//Hs.7019:AB005666
 F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107
 F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412
 F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:8
 8//Hs.40100:AB002390
 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2
 e-104:489:99//Hs.14409:AB011144
 F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451
 F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs
 .155464:AF088219
 F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853
 :X98054
 F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5
 e-105:773:82//Hs.23094:M19503
 F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902
 F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869

F-HEMBA1001526
 F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476
 F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580
 F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652
 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205
 F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814
 F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:AJ012449
 F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184
 F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228
 F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988
 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918
 F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210
 F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400
 F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870
 F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//0.038:198:64//Hs.34579:AI338536
 F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899
 F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204
 F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560
 F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283
 F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121
 F-HEMBA1001661
 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:669:99//Hs.107254:AC005943

F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0484//2.0e-57:447:79//Hs.158095:AB007953

F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788

F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060

F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760

F-HEMBA1001709//EST//0.85:131:65//Hs.131451:AI023995

F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:AI302836

F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114

F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL
PRECURSOR [Rattus norvegicus]//3.0e-30:195:92//Hs.132948:AA194452

F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554

F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101
524:U58197

F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363

F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415

F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:AI052250

F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37
:300:62//Hs.10887:AB013924

F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328

F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapien
s]//0.76:218:60//Hs.135553:N41598

F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//
Hs.98776:AC005622

F-HEMBA1001784//Homo sapiens mRNA for KIAA0474 protein, complete cds//6.
4e-09:265:67//Hs.158232:AB007943

F-HEMBA1001791

F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570

F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817

F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.

8e-07:439:59//Hs.266:U06233
 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0500//2.5e-175:809:98//Hs.118164:AB007969
 F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305
 F-HEMBA1001815
 F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA,
 partial cds//4.9e-80:842:70//Hs.158174:U66561
 F-HEMBA1001820//EST//0.057:214:62//Hs.148715:AI223845
 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//
 6.7e-42:510:65//Hs.66392:AF064244
 F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//
 5.2e-13:253:68//Hs.85313:AF071309
 F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//
 Hs.6151:D87078
 F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.155243:N70293
 F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:6
 8//Hs.6833:AB002324
 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.
 8e-185:865:98//Hs.78946:AB014517
 F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121
 F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSY
 LTRANSFERASE PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141
 922
 F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:3
 67:95//Hs.15423:T84036
 F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0484//5.4e-86:835:76//Hs.158095:AB007953
 F-HEMBA1001896
 F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds/

/0.43:114:71//Hs.6133:U94346
 F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633
 F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:200:62//Hs.9573:AF027302
 F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511
 F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141
 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:855:99//Hs.154934:AF000145
 F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295
 F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221
 F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882
 F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943
 F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360
 F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//Hs.25674:AF072242
 F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930
 F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive iso log of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178
 F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732
 F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100
 F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581
 F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palm aris et plantaris)//9.8e-09:294:63//Hs.99936:X14487

F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803:W63582
F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64
//Hs.78867:M93426
F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545
:U32907
F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827
F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057
F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776
F-HEMBA1002084
F-HEMBA1002092
F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) m
RNA, complete cds//5.6e-21:124:96//Hs.101842:L32832
F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09
:434:62//Hs.135102:AI190276
F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973
F-HEMBA1002119
F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802
F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393
F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:6
0//Hs.79170:D86980
F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6
e-06:353:62//Hs.23741:AB018263
F-HEMBA1002151
F-HEMBA1002153//EST//0.014:328:60//Hs.149115:AI244695
F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0507//5.6e-49:303:79//Hs.158241:AB007976
F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-
40:616:67//Hs.929:M57965

F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.4
4766:AJ007590

F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs
.155464:AF088219

F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//
Hs.114808:AF026245

F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141

F-HEMBA1002189//EST//5.1e-24:193:81//Hs.163161:AA778363

F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.2
7:382:59//Hs.21992:AB014589

F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0501//1.2e-14:199:72//Hs.159897:AB007970

F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696

F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767

F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculu
s]//1.6e-47:251:96//Hs.59906:AA001281

F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0488//2.4e-57:375:71//Hs.67619:AB007957

F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80/
/Hs.43681:AL022394

F-HEMBA1002237//EST//0.044:137:66//Hs.144448:AA812455

F-HEMBA1002241

F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887

F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, com
plete cds//1.1e-152:731:97//Hs.159564:AF061936

F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420

F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA,
complete cds//1.0:395:60//Hs.150926:AF017445

F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404

F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor m
RNA, complete cds//0.17:338:60//Hs.77729:AB010710

F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982

F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//
Hs.154326:D42087

F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8
e-187:872:98//Hs.6162:AB018314

F-HEMBA1002348//EST//1.0e-19:285:70//Hs.121860:AA776692

F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996

F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mR
NA, complete cds//2.4e-189:872:99//Hs.119023:AF092563

F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216

F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144

F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:
97//Hs.25527:AC005954

F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLI
C PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W271
41

F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.9079
8:U79289

F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMO
LOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561

F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.
sapiens]//1.3e-71:346:98//Hs.136121:W26490

F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160

F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit pr
ecursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783

F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:
92//Hs.154583:D50912

F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89
631:U48508

F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8
e-45:331:83//Hs.6189:AB011133

F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235

F-HEMBA1002495

F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161

F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74/
/Hs.19949:X98173

F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:46
0:83//Hs.113283:AF018080

F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.0e-159:738:98//Hs.6764:AJ011972

F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795

F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951

F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete
cds//6.1e-46:238:87//Hs.10458:AF088219

F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138
:655:98//Hs.68900:AF016903

F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//
Hs.102137:U31875

F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.000
20:603:57//Hs.20912:AB012162

F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205

F-HEMBA1002561//Human clone 23574 mRNA sequence//4.7e-17:268:72//Hs.7938
5:U90905

F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete
cds//4.3e-142:457:99//Hs.151411:AF075587

F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto

r, complete cds//2.8e-30:156:100//Hs.32170:AB015132
 F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159
 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363
 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4
 e-176:820:99//Hs.20141:AB011169
 F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.
 2e-189:632:97//Hs.91338:AB018351
 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65
 //Hs.125129:AB002334
 F-HEMBA1002629//Human density enhanced phosphatase-1 mRNA, complete cds/
 /1.3e-07:473:61//Hs.1177:U10886
 F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390
 F-HEMBA1002651
 F-HEMBA1002659//Human vascular endothelial growth factor related protein
 VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142
 F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4
 e-122:781:85//Hs.23094:M19503
 F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497
 F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368
 F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP ga
 ted 1 (alpha)//0.00096:418:61//Hs.1323:S42457
 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1)
 mRNA, partial cds//1.8e-11:541:60//Hs.124161:AF065164
 F-HEMBA1002696//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e
 -06:345:61//Hs.155647:AC004221
 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.
 0e-12:327:62//Hs.13245:AB007924
 F-HEMBA1002712

F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800
 F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7
 e-127:614:97//Hs.132942:AB014521
 F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGS
 T3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867
 F-HEMBA1002742//EST//0.97:138:60//Hs.160545:AI271596
 F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs
 .74061:X59372
 F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74/
 /Hs.40806:AA018786
 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817
 F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9
 e-178:834:98//Hs.74750:AB011126
 F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:4
 92:96//Hs.11833:AI299947
 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 m
 RNA, complete cds//3.9e-05:528:59//Hs.128208:U63809
 F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392
 F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326
 F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756
 F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938
 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cd
 s//3.4e-169:820:97//Hs.28307:AF071185
 F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744
 F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:73
 3:89//Hs.6059:AF093119
 F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:AI279904
 F-HEMBA1002833
 F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550

F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823

F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEE
D8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730

F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AI279429

F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679

F-HEMBA1002921

F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001

F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915

F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6
e-174:803:99//Hs.14687:AB011148

F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:G
enBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA1
30053

F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1
.1e-05:479:59//Hs.74019:X83703

F-HEMBA1002944//Human putative endothelin receptor type B-like protein m
RNA, complete cds//0.83:326:58//Hs.27747:U87460

F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.126762:AA913925

F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099

F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092

F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828

F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219

F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-
homolog phosphodiesterase E4)//1.5e-37:247:89//Hs.188:L20971

F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mR
NA, partial cds//1.7e-05:797:58//Hs.50758:AF092564

F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525

F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs
.155464:AF088219

F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486
 F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:33
 0:78//Hs.113283:AF018080
 F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.15942
 5:AJ001454
 F-HEMBA1003037//EST//0.53:59:74//Hs.148011:AI268003
 F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:33
 7:95//Hs.105907:AA186514
 F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-sub
 unit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182
 F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438
 F-HEMBA1003067
 F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1)
 mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164
 F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62
 //Hs.48998:AB007865
 F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454
 F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461
 F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881
 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721
 F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.
 musculus]//0.98:216:61//Hs.97865:AA405872
 F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721
 F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802
 F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//
 Hs.12432:AF070575
 F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.0
 38:288:63//Hs.6162:AB018314
 F-HEMBA1003136

F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279
 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99
 //Hs.63931:AJ005670
 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.
 1e-24:171:83//Hs.141874:AB014588
 F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740
 F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' r
 egion [E.coli]//4.7e-20:118:97//Hs.118831:AA211895
 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523
 F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135
 F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412
 F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:15
 4:85//Hs.113283:AF018080
 F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765
 F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784
 F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310
 F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012
 F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0005
 4:432:58//Hs.132206:AF039694
 F-HEMBA1003250
 F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, c
 omplete cds//4.3e-08:426:64//Hs.49585:AF075292
 F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991
 F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020
 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864
 F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867
 F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransfer
 ase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662
 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.

6e-167:799:98//Hs.12836:AB011109
 F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912
 F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160
 F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.105486:AA521012
 F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs.124224:AB001872
 F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459
 F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254
 F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328
 F-HEMBA1003330
 F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:78//Hs.146395:AB002329
 F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTG, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092
 F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159
 F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819
 F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637
 F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017
 F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552
 F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488
 F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813
 F-HEMBA1003403//Adducin 2 (beta) {alternative products} //5.0e-05:445:61//Hs.90951:U43959
 F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309
 F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546

F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962
 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:6
 86:99//Hs.25812:AF058696
 F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60/
 /Hs.47822:AB002378
 F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:77
 5:58//Hs.3847:U59632
 F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578
 F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.1
 6:321:60//Hs.13999:AB014600
 F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443
 F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:7
 8//Hs.22271:D26067
 F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811
 F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5
 .0e-75:736:73//Hs.505:U07559
 F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311
 F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6
 e-33:562:64//Hs.81469:U01833
 F-HEMBA1003556
 F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122
 F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327
 F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0
 e-58:455:66//Hs.101448:U35113
 F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972
 F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546
 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:1
 08:99//Hs.18420:AA599232
 F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:9

2//Hs.57937:W68285

F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405

F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827

F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916

F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory prote in HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782

F-HEMBA1003617//Homa sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344

F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF077954

F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750

F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159

F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudd ge ne product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591

F-HEMBA1003640//ESTs//1.1e-11:267:66//Hs.34359:AI122791

F-HEMBA1003645

F-HEMBA1003646

F-HEMBA1003656

F-HEMBA1003662

F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381

F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906

F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61 //Hs.79706:U53204

F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H. sapiens]//1.6e-100:478:98//Hs.118866:AI017072

F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5 e-74:606:77//Hs.9028:AF039691

F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187

F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.8
1:254:62//Hs.32316:AB011116

F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995

F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760

F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//
Hs.91916:AF035317

F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921

F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839

F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6
e-102:753:81//Hs.23094:M19503

F-HEMBA1003742//Homo sapiens chromosome 19, cosmid R31180//0.16:242:62//
Hs.153325:AC005390

F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946

F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//
Hs.8136:U81984

F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920

F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//1.7e-24:224
:81//Hs.18171:AA524327

F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172

F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064

F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3)
mRNA, complete cds//0.13:222:61//Hs.89230:AF031815

F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239

F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:
M88108

F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721

F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3
e-85:586:87//Hs.6051:AB014516

F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:AI204220

F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNIN
G ENTRY !!!! [H.sapiens] //3.8e-40:151:88//Hs.139007:H74314

F-HEMBA1003856//ESTs//8.6e-53:286:95//Hs.116645:AI005167

F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66/
/Hs.21355:AB002367

F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.
3e-30:580:63//Hs.27621:U52840

F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.895
63:D32002

F-HEMBA1003880

F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2
e-18:302:67//Hs.23711:AB018295

F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN
VMA7-RPS31A INTERGENIC REGION [S.cerevisiae] //1.2e-49:295:92//Hs.114673:
W72675

F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236

F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.0
81:345:58//Hs.78494:AB011097

F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:AI032875

F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:
69//Hs.154668:AB002389

F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562

F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis] //0
.0029:222:61//Hs.144236:W52380

F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055

F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:
66//Hs.2076:M29580

F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens] //2.1e-44:243:76//Hs.91146:N73230

F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567
F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965
F-HEMBA1003978
F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009
F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456
F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding
protein (FBI1) mRNA, complete cds//0.022:349:58//Hs.104640:AF000561
F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468
F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493
F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573
F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI379721
F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.
2e-51:359:84//Hs.15519:AB018315
F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI239930
F-HEMBA1004042//EST//0.00088:272:61//Hs.155763:AI312281
F-HEMBA1004045//EST//2.7e-20:408:66//Hs.162529:AA584160
F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M
60315
F-HEMBA1004049//ESTs//8.1e-68:430:86//Hs.146307:AA584638
F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//H
s.82837:L13435
F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, comp
lete cds//1.5e-46:199:80//Hs.46328:D87942
F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426
F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107
F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M2871
3
F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete
cds//4.3e-39:335:79//Hs.46468:U45984

F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:61//Hs.80712:D86957

F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064

F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI419759

F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343:62//Hs.5923:X82260

F-HEMBA1004143

F-HEMBA1004146

F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056

F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591:60//Hs.159277:AB018341

F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97//Hs.59988:AF067855

F-HEMBA1004199

F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI375427

F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays] //1.2e-35:205:94//Hs.10092:AI189282

F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040

F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748

F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514

F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans] //0.012:156:67//Hs.163588:AI073878

F-HEMBA1004238

F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571

F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522

F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295:72//Hs.56205:U96876

F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//Hs.83634:U52112

F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.
9e-73:490:77//Hs.141874:AB014588

F-HEMBA1004272

F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444

F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//
Hs.155313:AB002331

F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.
0:364:56//Hs.118738:AB018343

F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA
, complete cds//6.9e-187:868:99//Hs.101766:AF022795

F-HEMBA1004289

F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484

F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:AI270047

F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336314

F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//
Hs.69740:U09367

F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI204532

F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.
.017:209:64//Hs.43627:U35612

F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062

F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888

F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.
49:80:73//Hs.139648:AB014606

F-HEMBA1004341

F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cd
s//2.7e-39:270:86//Hs.80686:D89667

F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3
e-46:190:92//Hs.27424:U75968

F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.

3022:D85376

F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens] //7.8e-10:396:61//Hs.33688:AA020928

F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800

F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019

F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250

F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818

F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199

F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens] //1.4e-20:144:88//Hs.121076:AI246426

F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531

F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219

F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080

F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606

F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984

F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450

F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600

F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431

F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503

F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans] //1.4e-61:296:99//Hs.114622:AA693492

F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800

F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//H
s.76279:X53416
F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381
F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.
74:74:75//Hs.87497:U90552
F-HEMBA1004554
F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331
F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802
F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2
e-17:334:67//Hs.24536:AA479825
F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1e-35:337:78//Hs.78160:AF0
10238
F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661
F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft)
mRNA, complete cds//0.42:186:66//Hs.84136:U70370
F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606
F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198
F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178
F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416
F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891
F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780
F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522
F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083
F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796
F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582
F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141
F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252
F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.6

4:313:61//Hs.118578:X80821
F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73
//Hs.155174:AB007892
F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515
F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:
244:57//Hs.99975:X55019
F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328
:60//Hs.68900:AF016903
F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5
.9e-32:476:70//Hs.116874:AA524909
F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515
F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugatin
g enzyme E2 similar to Drosophila bendless gene product, complete cds//0
.16:329:58//Hs.75355:D83004
F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0
e-61:663:71//Hs.23094:M19503
F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813
F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504
F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.000
20:521:59//Hs.91400:AB006626
F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84/
/Hs.153563:AF011333
F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e
-24:416:65//Hs.76460:U49082
F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds
//1.2e-136:769:91//Hs.153088:L39060
F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.155657:M61120
F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5
e-115:909:78//Hs.23094:M19503

F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139

F-HEMBA1004771

F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235

F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106

F-HEMBA1004795

F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952

F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971

F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042

F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646

F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481

F-HEMBA1004847//ESTs//2.1e-09:66:98//Hs.158161:AA312511

F-HEMBA1004850//EST//0.033:253:64//Hs.158782:AI376601

F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150

F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987

F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077

F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633

F-HEMBA1004889//Growth arrest-specific 1//0.20:146:68//Hs.65029:L13698

F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304

F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106

F-HEMBA1004918//EST//0.78:122:61//Hs.145491:AI254348

F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172

F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X5

2947

F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959

F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331

F-HEMBA1004934

F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981

F-HEMBA1004954//ESTs//0.014:404:60//Hs.11177:AA417813

F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478

F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274

F-HEMBA1004972

F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:AB007914

F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946

F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013

F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750

F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589

F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026

F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429

F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356

F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548

F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560

F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237

F-HEMBA1005039//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627

F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, comple

te cds//0.078:442:59//Hs.100602:AF010193

F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802

F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462

F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587

F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381

F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785

F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105

F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561

F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916

F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304

F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106

F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875

F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021

F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216

F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914

F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197

F-HEMBA1005202

F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436

F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547

F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081

F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302

F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp

lete cds//6.0e-54:399:79//Hs.129735:AF010144
 F-HEMBA1005244//ESTs//2.5e-14:85:100//Hs.128744:AI191922
 F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896
 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7
 e-151:705:98//Hs.72660:AB011157
 F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380
 F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777
 F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//
 Hs.12451:U97018
 F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232
 F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs
 .155464:AF088219
 F-HEMBA1005311
 F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516
 F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615
 F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117
 F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.0007
 5:310:63//Hs.111597:U68723
 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:
 97//Hs.129361:AJ007581
 F-HEMBA1005353//EST//5.4e-09:222:68//Hs.119508:AA485732
 F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88/
 /Hs.151689:U09414
 F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.
 5e-70:572:73//Hs.43265:AF071787
 F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905
 F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mR
 NA//6.1e-43:341:81//Hs.154069:U06452
 F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI193053

F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448
 F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans] //1.0e-130:620:98//Hs.108990:N25951
 F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans] //7.7e-151:727:97//Hs.17118:AI033807
 F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513
 F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347
 F-HEMBA1005411
 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248
 F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323
 F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.89897:U28687
 F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783
 F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107
 F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368
 F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503
 F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219
 F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694
 F-HEMBA1005497//Glucocorticoid receptor alpha {alternative products} //8.7e-41:588:69//Hs.102761:U25029
 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:AC004957
 F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635

F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911
F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:
79//Hs.153014:AB002353
F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.mel
anogaster] //5.3e-76:378:97//Hs.22767:N99220
F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7
) gene, complete cds//0.54:623:56//Hs.143551:AF048693
F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575
F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.
1e-55:288:85//Hs.144563:AF057280
F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs
.155464:AF088219
F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cer
evisiae] //1.2e-30:166:96//Hs.17035:AI080471
F-HEMBA1005530
F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-ma
f) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376
F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461
F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903
F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257
F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507
F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9
e-128:610:98//Hs.77738:AB007932
F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873
F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64
//Hs.57929:AB011538
F-HEMBA1005582
F-HEMBA1005583
F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381

F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS//0.

54:439:59//Hs.2137:D49357

F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:5

7//Hs.7720:AB002323

F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609

F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982

F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.

2e-22:721:61//Hs.144563:AF057280

F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisi

ae] //1.8e-89:454:96//Hs.19400:AA662845

F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535

F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734

F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199

F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956

F-HEMBA1005666

F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.

7e-45:255:79//Hs.114293:AB011142

F-HEMBA1005679//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//

1.2e-37:356:77//Hs.139107:K00629

F-HEMBA1005680

F-HEMBA1005685

F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (E

plg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406

F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678

F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143

F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate sy

nthetase, dimethylallyltranstransferase, geranyltranstransferase)//2.6e-

20:151:88//Hs.77393:D14697

F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754

F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024
F-HEMBA1005755//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
1.8e-48:425:78//Hs.103948:K00627
F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs
.155464:AF088219
F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141
F-HEMBA1005813//ESTs//0.012:209:63//Hs.113365:R77747
F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds/
/2.0e-07:439:62//Hs.6133:U94346
F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577
F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788
F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9
e-42:690:66//Hs.23094:M19503
F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//H
s.79706:U53204
F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150
F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0484//1.4e-53:332:83//Hs.158095:AB007953
F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097
F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete
cds//7.2e-45:411:77//Hs.46468:U45984
F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.000
54:477:59//Hs.37125:U42766
F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081
F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HP
X42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006
F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger prot
ein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880
F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588

F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883
 F-HEMBA1005963
 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516
 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530
 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526
 F-HEMBA1006002
 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151
 F-HEMBA1006031
 F-HEMBA1006035
 F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080
 F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.141186:R99609
 F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.143321:AI139422
 F-HEMBA1006081
 F-HEMBA1006090//EST//1.2e-12:340:62//Hs.161195:AI418788
 F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313
 F-HEMBA1006100//ESTs//7.1e-22:273:73//Hs.144407:AA737799
 F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741
 F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968
 F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222
 F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372
 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734
 F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881
 F-HEMBA1006155
 F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575

F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627
F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117
F-HEMBA1006198//ESTs//0.017:133:67//Hs.142168:AA292540
F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98/
/Hs.109268:AF070557
F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.
7647:M94046
F-HEMBA1006252
F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706
F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.
00037:158:69//Hs.159277:AB018341
F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631
F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140
F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770
F-HEMBA1006283
F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964
F-HEMBA1006291
F-HEMBA1006293
F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA,
complete cds//0.76:416:58//Hs.46465:U45285
F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3
e-49:637:68//Hs.37656:AB011174
F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350
F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789
F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142
F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.mel
anogaster]//5.3e-76:378:97//Hs.22767:N99220
F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287
F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107

:X59244

F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026

F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.80667:AF010233

F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922

F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531

F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503

F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477

F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881

F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830

F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835

F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264

F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194

F-HEMBA1006445

F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889

F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369

F-HEMBA1006467

F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:AI091453

F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:AA875998

F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081

F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532

F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897

F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.128621:AA910431

F-HEMBA1006492

F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:AI248625
 F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389
 F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072
 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3
 e-141:470:98//Hs.153858:AB014566
 F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein]
 reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185
 F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002
 F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081
 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA
 , complete cds//4.4e-173:654:98//Hs.21301:AF093419
 F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638
 F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79
 //Hs.21490:AB007898
 F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425
 F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136
 F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.144372:AI346522
 F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479
 F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60
 //Hs.106387:AF029778
 F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs
 .155464:AF088219
 F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6
 e-38:441:69//Hs.23711:AB018295
 F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862
 F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875
 F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN
 SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI3
 91502

F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331
 F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589
 F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185
 F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003
 F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:U40282
 F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615
 F-HEMBA1006653
 F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189
 F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317
 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065
 F-HEMBA1006676
 F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575
 F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145
 F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198
 F-HEMBA1006708
 F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545
 F-HEMBA1006717//ESTs//2.6e-31:286:78//Hs.55573:W37226
 F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105
 F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087
 F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF035587

F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325

F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720

F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250

F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798

F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503

F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298

F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA287723

F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:AI051551

F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624

F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970

F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327

F-HEMBA1006865

F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN I N ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938

F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214

F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592

F-HEMBA1006914//EST//0.065:366:62//Hs.162914:AA666199

F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989

F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258

F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539
F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712
F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382
F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein/
/4.4e-92:437:98//Hs.42644:AJ010841
F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6
940:Z48633
F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete c
ds//1.8e-144:740:94//Hs.14934:AF004828
F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sia
lyltransferase//1.9e-79:447:89//Hs.75268:X74570
F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968
F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723
F-HEMBA1007002
F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282
F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mR
NA, complete cds//2.5e-78:827:70//Hs.43003:AF035812
F-HEMBA1007045
F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659
F-HEMBA1007052
F-HEMBA1007062
F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212
F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845
F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//
6.7e-75:417:91//Hs.80510:M74002
F-HEMBA1007080
F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-0
6:568:61//Hs.1974:M92432
F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA,

complete cds//0.95:541:57//Hs.3828:U49260
F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595
F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354
F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA643182
F-HEMBA1007129
F-HEMBA1007147//ESTs//3.2e-07:235:64//Hs.124813:W46172
F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136
F-HEMBA1007151
F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:97
//Hs.22396:AF062085
F-HEMBA1007178//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING
ENTRY !!!! [H.sapiens]//4.2e-39:248:90//Hs.157148:AA311921
F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965
F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.
6e-158:478:98//Hs.3363:D86987
F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252
F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6
e-177:839:98//Hs.27197:AB018340
F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan sy
ndrome)//2.7e-56:647:69//Hs.82314:M31642
F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//H
s.79706:U53204
F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:64//Hs.1
2432:AF070575
F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//
0.99:239:60//Hs.111749:U13695
F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836
F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H06475
F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529

F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637
 F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062
 F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74
 615
 F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506
 F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634
 F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241
 F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens] /
 /3.5e-09:144:76//Hs.20597:W58370
 F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130
 F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006
 F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561
 F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568
 F-HEMBA1000008//H.sapiens mRNA for translin associated protein X//1.1e-4
 3:370:78//Hs.96247:X95073
 F-HEMBA1000018//Nuclear factor of kappa light polypeptide gene enhancer
 in B-cells 1 (p105)//1.0:108:70//Hs.83428:M58603
 F-HEMBA1000024//EST//5.4e-07:137:70//Hs.125389:AA878307
 F-HEMBA1000025//EST//0.99:362:58//Hs.121221:AA757392
 F-HEMBA1000030//H.sapiens mRNA for cylicin II//1.3e-10:525:62//Hs.3232:Z
 46788
 F-HEMBA1000036
 F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, c
 omplete cds//6.2e-102:450:98//Hs.20815:AF084928
 F-HEMBA1000039//EST//0.0034:97:73//Hs.141684:W35358
 F-HEMBA1000044//ESTs//0.0048:218:63//Hs.123161:AA807319
 F-HEMBA1000048//EST//0.00025:222:62//Hs.122474:AA765131
 F-HEMBA1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717
 F-HEMBA1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3

e-54:259:88//Hs.23094:M19503
F-HEM BB1000055//ESTs//0.0017:289:62//Hs.125755:AA286923
F-HEM BB1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9
e-59:286:84//Hs.93121:AB018304
F-HEM BB1000083
F-HEM BB1000089//EST//0.0016:192:66//Hs.137093:AA917621
F-HEM BB1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645
F-HEM BB1000103//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
4.9e-43:418:74//Hs.103948:K00627
F-HEM BB1000113//EST//4.6e-23:221:76//Hs.142065:AA173763
F-HEM BB1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521
F-HEM BB1000136//ESTs//2.3e-101:507:96//Hs.12659:AA195207
F-HEM BB1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044
F-HEM BB1000144//EST//4.5e-52:298:91//Hs.149580:AI281881
F-HEM BB1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:
X92715
F-HEM BB1000175//EST//1.0:101:65//Hs.162898:AA659646
F-HEM BB1000198//EST//0.99:179:56//Hs.116880:AA662457
F-HEM BB1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4
e-15:139:82//Hs.101414:AB011129
F-HEM BB1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277
F-HEM BB1000218//EST//0.11:136:63//Hs.134683:AI092013
F-HEM BB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X6
9962
F-HEM BB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y
08612
F-HEM BB1000244//ESTs//3.2e-15:139:81//Hs.134549:AI078483
F-HEM BB1000250//Homo sapiens protein associated with Myc mRNA, complete
cds//2.1e-156:735:98//Hs.151411:AF075587

F-HEMBB1000258//EST//0.0091:325:60//Hs.97533:AA435884
 F-HEMBB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4
 e-33:100:100//Hs.27424:U75968
 F-HEMBB1000266//Homo sapiens mRNA for myosin phosphatase target subunit
 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930
 F-HEMBB1000272//ESTs//1.3e-93:440:99//Hs.109224:N46684
 F-HEMBB1000274//ESTs//0.41:221:65//Hs.71990:AA151796
 F-HEMBB1000284//EST//0.00024:108:73//Hs.100725:F13689
 F-HEMBB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574
 F-HEMBB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.
 00092:252:65//Hs.41153:AB018326
 F-HEMBB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787
 F-HEMBB1000318//EST//0.014:184:61//Hs.155758:AI311870
 F-HEMBB1000335//EST//0.99:187:63//Hs.137424:AA243729
 F-HEMBB1000336//EST//1.0:209:63//Hs.150410:AI003611
 F-HEMBB1000337//EST//0.086:133:66//Hs.128207:AA972330
 F-HEMBB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127
 F-HEMBB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:76//Hs
 .155464:AF088219
 F-HEMBB1000341
 F-HEMBB1000343//EST//0.66:163:63//Hs.150822:AI302729
 F-HEMBB1000354//ESTs//7.1e-61:292:100//Hs.152266:AA926874
 F-HEMBB1000369//ESTs, Highly similar to t-BOP [M.musculus]//0.013:157:64
 //Hs.129982:AI420970
 F-HEMBB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934
 F-HEMBB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348
 F-HEMBB1000391//ESTs//0.033:237:64//Hs.135289:AI092963
 F-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4
 e-165:762:98//Hs.16184:AJ001642

F-HEMBB1000402//EST//0.013:291:59//Hs.149191:AI246155
 F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194
 F-HEMBB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925
 F-HEMBB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.129735:AF010144
 F-HEMBB1000438//ESTs//0.073:446:58//Hs.134632:AI223429
 F-HEMBB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627
 F-HEMBB1000449//EST//5.5e-21:356:67//Hs.157848:AI362501
 F-HEMBB1000455//ESTs//0.092:147:65//Hs.106446:N93227
 F-HEMBB1000472
 F-HEMBB1000480//EST//0.98:83:71//Hs.146462:AI124898
 F-HEMBB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206
 F-HEMBB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560
 F-HEMBB1000491
 F-HEMBB1000493//ESTs//0.019:103:69//Hs.138358:T66178
 F-HEMBB1000510//Glucocorticoid receptor alpha {alternative products} //1.6e-46:409:77//Hs.102761:U25029
 F-HEMBB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413
 F-HEMBB1000523//ESTs//0.69:332:59//Hs.106845:W19543
 F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710
 F-HEMBB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//7.7e-31:554:67//Hs.157142:U85996
 F-HEMBB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.158095:AB007953
 F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:65//Hs.5444:AB018293
 F-HEMBB1000564
 F-HEMBB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001

F-HEMBB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238

F-HEMBB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533

F-HEMBB1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091

F-HEMBB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990

F-HEMBB1000592//EST//0.0038:51:88//Hs.148022:AI269323

F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356

F-HEMBB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589

F-HEMBB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809

F-HEMBB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864

F-HEMBB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481

F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349

F-HEMBB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075

F-HEMBB1000638//EST//0.0076:92:75//Hs.125496:AA883735

F-HEMBB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830

F-HEMBB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778

F-HEMBB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531

F-HEMBB1000665//EST//0.44:152:63//Hs.149534:AI280924

F-HEMBB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2

e-79:280:85//Hs.23094:M19503
F-HEMBB1000673//ESTs//0.99:177:59//Hs.149864:N80474
F-HEMBB1000684//Protein kinase, interferon-inducible double stranded RNA
dependent//2.6e-31:220:87//Hs.73821:M35663
F-HEMBB1000693//Homo sapiens neuroan1 mRNA, complete cds//5.3e-120:575:9
7//Hs.158300:AF040723
F-HEMBB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125
F-HEMBB1000706//EST//8.6e-14:373:61//Hs.138281:R55703
F-HEMBB1000709//EST//0.99:110:65//Hs.162437:AA577510
F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56
741
F-HEMBB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216
F-HEMBB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328
F-HEMBB1000749//EST//3.1e-42:271:87//Hs.162197:AA535216
F-HEMBB1000763
F-HEMBB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.
melanogaster]//0.021:111:72//Hs.38178:AA921830
F-HEMBB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5e-116:580:
97//Hs.5009:AA081390
F-HEMBB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//H
s.86201:U78876
F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//3.
0e-65:672:71//Hs.155983:AB014577
F-HEMBB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727
F-HEMBB1000794//ESTs//0.00098:289:59//Hs.138782:N73572
F-HEMBB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375
F-HEMBB1000810//ESTs//0.038:92:71//Hs.148763:AA668871
F-HEMBB1000821//EST//0.94:129:62//Hs.162299:AA555154
F-HEMBB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421

F-HEMBB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069
F-HEMBB1000827
F-HEMBB1000831
F-HEMBB1000835//EST//4.3e-27:201:85//Hs.141451:N29915
F-HEMBB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948
F-HEMBB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4
e-135:875:85//Hs.23094:M19503
F-HEMBB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:
61//Hs.311:U00238
F-HEMBB1000870//EST//0.00091:246:62//Hs.126502:AA913831
F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//
Hs.128434:AF085351
F-HEMBB1000883//ESTs//0.42:107:67//Hs.154173:AI379823
F-HEMBB1000887
F-HEMBB1000888//ESTs//1.0:137:67//Hs.8121:AA521290
F-HEMBB1000890//ESTs//1.0:116:65//Hs.7105:T23433
F-HEMBB1000893//EST//0.0079:408:58//Hs.146504:AI129834
F-HEMBB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875
F-HEMBB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//
Hs.7938:D86984
F-HEMBB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049
F-HEMBB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468
F-HEMBB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089
F-HEMBB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593
F-HEMBB1000947
F-HEMBB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9
.3e-48:572:72//Hs.2379:U23942
F-HEMBB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938
F-HEMBB1000975//ESTs//0.78:180:66//Hs.104789:AA417124

F-HEMBB1000981

F-HEMBB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.122967:AF059569

F-HEMBB1000991//EST//0.12:125:66//Hs.22945:R43713

F-HEMBB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055

F-HEMBB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004:AB014565

F-HEMBB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025

F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604:AC002310

F-HEMBB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991

F-HEMBB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247

F-HEMBB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:AI420970

F-HEMBB1001037//EST//0.0057:192:66//Hs.149987:AI291177

F-HEMBB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721

F-HEMBB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586

F-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832:AB014518

F-HEMBB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:AF088219

F-HEMBB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942

F-HEMBB1001063

F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803

F-HEMBB1001096//EST//0.017:154:66//Hs.130403:AA909272

F-HEMBB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293

F-HEMBB1001105//Human BRCA2 region, mRNA sequence CG016//0.30:84:75//Hs.
112434:U50529

F-HEMBB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61
ALPHA SUBUNIT [*Canis familiaris*]//9.3e-38:341:77//Hs.14038:R06800

F-HEMBB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062

F-HEMBB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139

F-HEMBB1001119

F-HEMBB1001126

F-HEMBB1001133//H.sapiens mRNA for translin associated protein X//1.2e-2
8:739:61//Hs.96247:X95073

F-HEMBB1001137

F-HEMBB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:
69//Hs.146395:AB002329

F-HEMBB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854

F-HEMBB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716

F-HEMBB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863

F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:
66//Hs.73073:D78334

F-HEMBB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CON
TAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [*S.cerevisiae*]//1.5e-65:
312:100//Hs.86878:AA599183

F-HEMBB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:1
99:64//Hs.74047:X71129

F-HEMBB1001199

F-HEMBB1001208//ESTs//0.12:120:69//Hs.130093:AA928802

F-HEMBB1001209//EST//0.00028:215:65//Hs.118276:W15258

F-HEMBB1001210//EST//2.9e-05:297:60//Hs.88840:AA281452

F-HEMBB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5
e-37:260:76//Hs.72660:AB011157

F-HEMBB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0507//0.00046:650:58//Hs.158241:AB007976

F-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [M
us musculus]//6.7e-103:477:100//Hs.127835:AI378790

F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:6
7//Hs.129918:AB005754

F-HEMBB1001249//EST//0.26:203:63//Hs.140791:AA935909

F-HEMBB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219

F-HEMBB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977

F-HEMBB1001267//Ataxia telangiectasia mutated (includes complementation
groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828

F-HEMBB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248

F-HEMBB1001282//GA-binding protein transcription factor, beta subunit 2
(47kD)//0.39:531:57//Hs.78915:U13045

F-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK
353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.1660
6:W81021

F-HEMBB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890

F-HEMBB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sap
iens]//1.3e-135:654:98//Hs.124217:AA020848

F-HEMBB1001302

F-HEMBB1001304//ESTs//0.98:109:68//Hs.138972:AA047725

F-HEMBB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339

F-HEMBB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs
.155464:AF088219

F-HEMBB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7
e-98:625:85//Hs.23094:M19503

F-HEMBB1001326//ESTs//0.00030:257:63//Hs.62208:H12380

F-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:8

7//Hs.43071:AA206222

F-HEMBB1001335

F-HEMBB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.

5e-56:282:87//Hs.15731:AB011135

F-HEMBB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:

161:65//Hs.132206:AF039694

F-HEMBB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878

F-HEMBB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.

2e-45:176:77//Hs.114293:AB011142

F-HEMBB1001356//EST//0.32:292:59//Hs.135771:AI005648

F-HEMBB1001364

F-HEMBB1001366//EST//7.8e-24:367:69//Hs.138765:N70347

F-HEMBB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs

.155464:AF088219

F-HEMBB1001369//EST//0.17:211:63//Hs.120066:AA707973

F-HEMBB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2

e-36:225:79//Hs.129748:AB011099

F-HEMBB1001384

F-HEMBB1001387//ESTs//0.61:215:60//Hs.145915:AI342230

F-HEMBB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8

e-94:568:83//Hs.23094:M19503

F-HEMBB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete

cds//0.021:373:58//Hs.125750:AF065988

F-HEMBB1001424//EST//0.20:307:58//Hs.135336:AI049827

F-HEMBB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//

Hs.83466:AF038174

F-HEMBB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos tau

rus]//5.5e-153:729:96//Hs.21679:AF034175

F-HEMBB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:

85//Hs.101996:AB002345
 F-HEMBB1001443
 F-HEMBB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216
 F-HEMBB1001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038
 F-HEMBB1001458//EST//1.7e-09:106:83//Hs.141422:N20920
 F-HEMBB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220
 F-HEMBB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740
 F-HEMBB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303
 F-HEMBB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088
 F-HEMBB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942
 F-HEMBB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815
 F-HEMBB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735
 F-HEMBB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093
 F-HEMBB1001536//ESTs//0.0047:120:68//Hs.144858:R67748
 F-HEMBB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306
 F-HEMBB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315
 F-HEMBB1001562//ESTs//0.95:161:61//Hs.145075:AI208240
 F-HEMBB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953
 F-HEMBB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080

F-HEM BB1001585

F-HEM BB1001586//EST//0.84:132:64//Hs.145264:AI218708

F-HEM BB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.9079
8:U79289

F-HEM BB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414

F-HEM BB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680

F-HEM BB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314

F-HEM BB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713

F-HEM BB1001635//ESTs//0.92:282:60//Hs.126980:AA934077

F-HEM BB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.
116549:AL009172

F-HEM BB1001641//EST//0.11:53:81//Hs.112445:AA594279

F-HEM BB1001653//EST//0.91:124:64//Hs.144213:T40480

F-HEM BB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds
//7.0e-13:473:63//Hs.54481:D86407

F-HEM BB1001668//ESTs//0.94:83:69//Hs.146202:AI252519

F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.
3e-172:803:98//Hs.24439:AB014546

F-HEM BB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:1
00//Hs.106104:AA599496

F-HEM BB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430

F-HEM BB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6
e-08:425:62//Hs.37035:U07664

F-HEM BB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398

F-HEM BB1001706

F-HEM BB1001707//EST//0.091:241:60//Hs.136830:AA769219

F-HEM BB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064

F-HEM BB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs
.155464:AF088219

F-HEMBB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485
:97//Hs.120581:W25578

F-HEMBB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244

F-HEMBB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144

F-HEMBB1001753//ESTs//0.00013:35:100//Hs.139643:H06263

F-HEMBB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077

F-HEMBB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639

F-HEMBB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0507//2.9e-13:498:60//Hs.158241:AB007976

F-HEMBB1001785//EST//0.16:262:60//Hs.162526:AA584102

F-HEMBB1001797//ESTs//0.37:201:63//Hs.91559:AA806370

F-HEMBB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951

F-HEMBB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0487//1.3e-54:311:81//Hs.92381:AB007956

F-HEMBB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017

F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCI
P1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209

F-HEMBB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190

F-HEMBB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:8
6//Hs.22271:D26067

F-HEMBB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370

F-HEMBB1001850//EST//0.0035:204:61//Hs.7311:T23858

F-HEMBB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs
.155464:AF088219

F-HEMBB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752

F-HEMBB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371

F-HEMBB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503

F-HEMBB1001872

F-HEMBB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923
:Y12478

F-HEMBB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box
protein)//0.32:346:60//Hs.100555:X98743

F-HEMBB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868

F-HEMBB1001899//ESTs//0.17:242:62//Hs.136969:AA830918

F-HEMBB1001905

F-HEMBB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155

F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA
, complete cds//1.2e-83:672:81//Hs.82210:U47742

F-HEMBB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62
//Hs.159777:Z19955

F-HEMBB1001911

F-HEMBB1001915//ESTs//0.92:136:71//Hs.144465:R68882

F-HEMBB1001921//EST//2.0e-19:398:67//Hs.44789:N36113

F-HEMBB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245

F-HEMBB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398

F-HEMBB1001930//EST//0.043:157:63//Hs.161927:AA483904

F-HEMBB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:8
0//Hs.154326:D42087

F-HEMBB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875

F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:6
6//Hs.40100:AB002390

F-HEMBB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:3
84:60//Hs.8546:U97669

F-HEMBB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101

F-HEMBB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//H
s.96:D90070

F-HEMBB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418

F-HEMBB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053

F-HEMBB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969

F-HEMBB1001973//Myelin oligodendrocyte glycoprotein {alternative products} //2.1e-48:426:78//Hs.53217:Z48051

F-HEMBB1001983

F-HEMBB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051

F-HEMBB1001990//ESTs//0.25:171:64//Hs.7961:AA401205

F-HEMBB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103

F-HEMBB1001997//EST//5.3e-33:294:76//Hs.161041:H82636

F-HEMBB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964

F-HEMBB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093

F-HEMBB1002009//ESTs//0.066:441:58//Hs.125313:AI201685

F-HEMBB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951

F-HEMBB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699

F-HEMBB1002043//ESTs, Weakly similar to T06E6.d [C.elegans] //1.0:217:60//Hs.3487:AA425553

F-HEMBB1002044

F-HEMBB1002045

F-HEMBB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256

F-HEMBB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661

F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512

F-HEMBB1002069

F-HEMBB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239

F-HEMBB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625

F-HEMBB1002115//EST//0.0083:244:64//Hs.125353:AA877080
 F-HEMBB1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027
 F-HEMBB1002139//ESTs//0.64:145:71//Hs.157821:AI362013
 F-HEMBB1002142//ESTs//0.013:311:59//Hs.150037:AI292214
 F-HEMBB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254
 F-HEMBB1002189//EST//0.26:81:70//Hs.147726:AI220208
 F-HEMBB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.1
 6:608:58//Hs.4:X03350
 F-HEMBB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//H
 s.301:U18934
 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:40
 5:67//Hs.104115:X52332
 F-HEMBB1002218//EST//0.015:241:61//Hs.105298:AA489813
 F-HEMBB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs
 .155464:AF088219
 F-HEMBB1002247
 F-HEMBB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HP
 X42B) mRNA, complete cds//6.8e-47:418:77//Hs.125231:AF068006
 F-HEMBB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0
 e-47:437:77//Hs.154872:AB011166
 F-HEMBB1002255//ESTs//0.017:255:61//Hs.126786:U74314
 F-HEMBB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA,
 complete cds//0.17:511:57//Hs.58169:AF017790
 F-HEMBB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998
 F-HEMBB1002300
 F-HEMBB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete
 cds//6.3e-14:228:72//Hs.46468:U45984
 F-HEMBB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083
 F-HEMBB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:39

9:96//Hs.105837:AA536054
 F-HEMBB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188
 F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein/
 /1.4e-155:724:98//Hs.42644:AJ010841
 F-HEMBB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991
 F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//
 1.7e-06:66:96//Hs.154762:U00943
 F-HEMBB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838
 F-HEMBB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796
 F-HEMBB1002381
 F-HEMBB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//H
 s.2126:L36566
 F-HEMBB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784
 F-HEMBB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456
 F-HEMBB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0501//2.0e-32:371:73//Hs.159897:AB007970
 F-HEMBB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.544
 86:X54150
 F-HEMBB1002442
 F-HEMBB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:7
 7//Hs.154326:D42087
 F-HEMBB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101
 F-HEMBB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274
 F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-
 89:493:92//Hs.159605:U43885
 F-HEMBB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA,
 complete cds//0.019:228:63//Hs.74304:AF001691
 F-HEMBB1002492//EST//0.24:149:62//Hs.146790:AI149051
 F-HEMBB1002495//Fc fragment of IgE, high affinity I, receptor for; beta

polypeptide//1.3e-22:331:71//Hs.30:M89796
F-HEM BB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494
F-HEM BB1002509//ESTs//0.017:220:63//Hs.155263:AI273725
F-HEM BB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354
F-HEM BB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4
e-50:580:72//Hs.23094:M19503
F-HEM BB1002522//EST//0.010:172:62//Hs.147224:AI205719
F-HEM BB1002531
F-HEM BB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs
.155464:AF088219
F-HEM BB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102
F-HEM BB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648
F-HEM BB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191
F-HEM BB1002579//EST//1.0:77:68//Hs.147935:AI250286
F-HEM BB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095
F-HEM BB1002590//ESTs//0.64:132:63//Hs.155688:AI003657
F-HEM BB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336
F-HEM BB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-15
2:710:98//Hs.129826:AF089749
F-HEM BB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817
F-HEM BB1002603//EST//0.10:144:63//Hs.158180:AI367945
F-HEM BB1002607//ESTs//0.024:345:62//Hs.143304:AI084058
F-HEM BB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323
F-HEM BB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711
F-HEM BB1002614//ESTs//0.0048:136:71//Hs.106280:R13901
F-HEM BB1002617//EST//0.034:320:59//Hs.41223:H89127
F-HEM BB1002623//ESTs//0.88:222:60//Hs.129920:AA167217
F-HEM BB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs
.151051:U07620

F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811
 F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680
 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679
 F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124
 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674
 F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504
 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992
 F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor
 (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614
 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588
 F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN
 SUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae] //0.0048:84:83//Hs
 .20814:AI242922
 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729
 F-MAMMA1000009//Human c-yes-1 mRNA//1.0e-48:447:77//Hs.75680:M15990
 F-MAMMA1000019
 F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750
 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945
 F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739
 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461
 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculu
 s] //2.7e-18:330:63//Hs.59906:AA001281
 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF
 F40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019
 F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840
 F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:7
 0//Hs.22271:D26067
 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0
 0013:199:69//Hs.37656:AB011174

F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA
 , complete cds//1.2e-52:346:77//Hs.90357:U40705

F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792

F-MAMMA1000117

F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508

F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402

F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319

F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843

F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585

F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924

F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050

F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695

F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530

F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657

F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739

F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035

F-MAMMA1000227//ESTs//0.010:268:60//Hs.116412:AA506926

F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913

F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873

F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587

F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543

F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015

F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874
 F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:8
 7//Hs.154326:D42087
 F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65
 //Hs.1376:U26726
 F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361
 F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:
 341:68//Hs.2161:M62505
 F-MAMMA1000284
 F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:8
 4//Hs.154326:D42087
 F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641
 F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:5
 10:57//Hs.75813:L33243
 F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529
 F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519
 F-MAMMA1000313
 F-MAMMA1000331
 F-MAMMA1000339
 F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN
 STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//
 Hs.13096:AA180963
 F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72
 //Hs.155174:AB007892
 F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0484//3.7e-24:233:72//Hs.158095:AB007953
 F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0
 e-75:498:85//Hs.23094:M19503
 F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:8

5//Hs.154326:D42087
 F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569
 F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like facto
 r, complete cds//1.2e-149:710:98//Hs.32170:AB015132
 F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330
 :60//Hs.82208:L46590
 F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4
 e-58:834:68//Hs.23094:M19503
 F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) m
 RNA, complete cds//1.2e-08:117:84//Hs.83916:U53468
 F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725
 F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092
 F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09
 F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111
 F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532
 F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0
 .98:553:56//Hs.19492:AF061573
 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459
 F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641
 F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//
 5.1e-48:491:72//Hs.12102:AF034546
 F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.
 51048:X68830
 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1
 e-39:342:78//Hs.154872:AB011166
 F-MAMMA1000446
 F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-bindin
 g protein [C.elegans]//5.1e-08:58:93//Hs.9043:W21827

F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818

F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830

F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830

F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948

F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482

F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219

F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878

F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352

F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497

F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352

F-MAMMA1000565

F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//5.8e-51:404:80//Hs.125231:AF068006

F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045

F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780

F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390:78//Hs.159523:AF001622

F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744

F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886

F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519

F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091

:300:60//Hs.29207:AF071494
 F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478
 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605
 F-MAMMA1000623
 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.
 98614:AF006751
 F-MAMMA1000643//Homo sapiens nephrocytin (NPHP1) mRNA, partial cds//0.0
 92:365:59//Hs.75474:AF023674
 F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353
 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//
 9.0e-30:531:64//Hs.139107:K00629
 F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490
 F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4
 316:U80743
 F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds
 //3.3e-07:249:62//Hs.44481:U13220
 F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627
 F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081
 F-MAMMA1000713//Acetylcholinesterase {I4-E5 doman} [human, tumor cell li
 nes, Genomic, 847 nt]//0.16:84:72//Hs.157124:S71129
 F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:61//Hs.274
 14:U79275
 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-
 07:210:66//Hs.71148:AA854648
 F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247
 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8
 .1e-22:288:72//Hs.114685:AA700024
 F-MAMMA1000731//Homo sapiens CHD1. mRNA, complete cds//1.5e-23:292:66//Hs
 .22670:AF006513

F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0484//4.8e-40:288:78//Hs.158095:AB007953

F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//
Hs.1742:L33075

F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:
802:98//Hs.31575:AF100141

F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580

F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.
3e-51:323:88//Hs.153468:AB011147

F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494

F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-1
4:285:68//Hs.162011:AA513663

F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative product
s} //6.2e-47:341:82//Hs.53217:Z48051

F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNIN
G ENTRY !!!! [H.sapiens]//9.8e-19:131:76//Hs.118972:AA761369

F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288

F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114

F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137

F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//
Hs.12432:AF070575

F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849

F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130

F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089

F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e-48:241:74//Hs
.155464:AF088219

F-MAMMA1000841

F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA

, complete cds//0.18:483:59//Hs.82210:U47742
 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696
 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877
 F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022
 F-MAMMA1000855
 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:3
 20:59//Hs.71388:AF032906
 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135
 F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342
 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.
 116549:AL009172
 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812
 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59/
 /Hs.75850:D87459
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//1.4e-91:484:94//Hs.138938:AA012894
 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy c
 hain H3//2.6e-06:211:63//Hs.76716:X67055
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683
 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239
 F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA,
 3429 nt]//1.0e-25:312:66//Hs.116007:S79267

F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968
F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 compo-
nt of branched chain keto acid dehydrogenase complex)//1.8e-38:395:71//H
s.89479:X66785
F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734
F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63
//Hs.83790:AB002303
F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:
566:64//Hs.25640:AB000714
F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474
F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, comp-
lete cds//1.1e-56:310:85//Hs.129735:AF010144
F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814
F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096
F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802
F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062
F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007
F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724
F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711
F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds
//4.7e-17:100:100//Hs.13451:Y15718
F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968
F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA
, complete cds//3.6e-32:753:61//Hs.98384:AF062006
F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857
F-MAMMA1001038
F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//H
s.119000:M95178
F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882

F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719

F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503

F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585

F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116

F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749.

F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503

F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420

F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896

F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254

F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627

F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045

F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915

F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219

F-MAMMA1001133

F-MAMMA1001139

F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534

F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217

F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741

F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147

F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299
 F-MAMMA1001181
 F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA,
 complete cds//6.5e-47:313:81//Hs.97203:U83171
 F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083
 F-MAMMA1001198
 F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348
 F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974
 F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776
 F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200
 F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:8
 4//Hs.154326:D42087
 F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8
 e-05:435:59//Hs.30898:AB014534
 F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587
 F-MAMMA1001244
 F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476
 F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121
 F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149
 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.
 8e-41:659:64//Hs.65238:AB014561
 F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7
 e-33:336:74//Hs.23094:M19503
 F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//H
 s.21858:U80747
 F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:7
 6//Hs.74554:D38522
 F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832

F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998

F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426

F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305

F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//1.9e-58:295:97//Hs.102336:Z83838

F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087

F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147

F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806

F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197

F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267

F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258

F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:80//Hs.42674:U61981

F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR//4.6e-09:415:58//Hs.839:M86826

F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:D83402

F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763

F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:64//Hs.82001:U50928

F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:AL022394

F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//0.00042:125:75//Hs.46328:D87942

F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:54
3:71//Hs.37181:D64108

F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321

F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590

F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040

F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053

F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//
2.0e-24:273:72//Hs.75939:D78335

F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3
.2e-25:397:68//Hs.116874:AA524909

F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366

F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0
.99:258:61//Hs.154196:U87269

F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795

F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506

F-MAMMA1001547

F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5
e-130:614:98//Hs.129937:AB007931

F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.
sapiens]//0.71:181:62//Hs.118866:AI017072

F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M6
1764

F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339

F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132

F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375

F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23
642:U79266

F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152

F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.1

58229:U28727

F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055//1.4e-40:447:73//Hs.154353:AL022165

F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796

F-MAMMA1001635

F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524

F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140:68//Hs.59829:AB014602

F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349:AB007917

F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens] //0.064:472:60//Hs.110819:AI027548

F-MAMMA1001671

F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317

F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889

F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765

F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549

F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete cds//8.0e-45:323:83//Hs.46468:U45984

F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548

F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926

F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs.159154:U47634

F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098
 F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768
 F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245
 F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7
 e-67:822:69//Hs.23094:M19503
 F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOH
 01) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632
 F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822
 F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109
 F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcr
 ipt, partial//6.6e-41:309:84//Hs.102576:AJ010230
 F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072
 F-MAMMA1001768//Human transcription factor, forkhead related activator 4
 (FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF042832
 F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:68
 6:79//Hs.113283:AF018080
 F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//
 0.00071:392:60//Hs.32981:U38276
 F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940
 F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549
 F-MAMMA1001788//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
 6.7e-21:212:77//Hs.103948:K00627
 F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72/
 /Hs.5158:AB007869
 F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987
 F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884
 F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096
 F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582
 F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589

F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//Hs.114948:AF059293

F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742

F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691

F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs.56808:D88827

F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665

F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028

F-MAMMA1001854

F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218

F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060

F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.084:672:58//Hs.152455:AF044209

F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687

F-MAMMA1001878

F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944

F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576

F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078

F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521

F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874

F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529

F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859

F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//Hs.91916:AF035317

F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878

F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sapiens]//7.9e-09:150:72//Hs.118222:N91115

F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633

F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826

F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915
 F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159
 F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0484//1.2e-54:455:70//Hs.158095:AB007953
 F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580
 F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225
 F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256
 F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305
 F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5
 e-36:382:75//Hs.23094:M19503
 F-MAMMA1002078
 F-MAMMA1002082
 F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012
 F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partia
 l//0.54:388:57//Hs.99423:AJ010840
 F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120
 F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932
 F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs
 .155464:AF088219
 F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:AI272963
 F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638
 F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338
 F-MAMMA1002145//EST//0.12:204:60//Hs.160983:AI392837
 F-MAMMA1002153
 F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97/
 /Hs.88424:AA281385
 F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD
 61)//0.99:310:58//Hs.87149:M35999
 F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196

F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X172
06

F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:
U39400

F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:1
21:98//Hs.146354:Z22548

F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362

F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120

F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk5
2b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:AI024063

F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gam
ma subunit [R.norvegicus]//4.6e-69:344:90//Hs.76822:AI359536

F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, co
mplete cds//0.99:454:56//Hs.122755:AF032986

F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903

F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:AI308841

F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, compl
ete cds//1.2e-06:427:61//Hs.69949:M94172

F-MAMMA1002269

F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715

F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440

F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF
F40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019

F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, comp
lete cds//4.3e-07:349:64//Hs.92614:M62302

F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460

F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57
//Hs.77234:AB001914

F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935
 F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens] //6.9e-41:293:83//Hs.105292:AA504776
 F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA,
 complete cds//0.0037:173:67//Hs.69423:AF055481
 F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0487//1.8e-41:473:65//Hs.92381:AB007956
 F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291
 F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908
 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//
 Hs.133342:AF070536
 F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515
 F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPI
 P8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026
 F-MAMMA1002332//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//
 1.2e-26:342:72//Hs.103948:K00627
 F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.
 8e-07:669:58//Hs.5333:AB018254
 F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6
 940:Z48633
 F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING
 ENTRY !!!! [H.sapiens] //3.9e-14:146:81//Hs.163073:R02591
 F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907
 F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086
 F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539
 F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78
 //Hs.32511:AB007901
 F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733
 F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818

F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830
 F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923
 F-MAMMA1002362//EST//0.25:304:58//Hs.162427:AA576345
 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34
 677
 F-MAMMA1002384//ESTs//1.1e-05:220:65//Hs.141388:R52022
 F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-11
 8:578:97//Hs.25516:AI086362
 F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624
 F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632
 F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737
 F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745
 F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788
 F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030
 F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:8
 3//Hs.154326:D42087
 F-MAMMA1002446
 F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809
 F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6
 .3e-06:595:59//Hs.99932:L38707
 F-MAMMA1002470
 F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, comple
 te cds//0.018:417:58//Hs.75074:U12779
 F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds/
 /9.4e-120:560:98//Hs.155223:AF055460
 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628
 F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]
 //4.0e-07:257:63//Hs.133013:AA604920

F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391
:L12392

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214

F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788

F-MAMMA1002554

F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:1
87:62//Hs.62354:M83822

F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421

F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368

F-MAMMA1002573//ESTs//2.1e-48:265:94//Hs.155128:AI224516

F-MAMMA1002585

F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831

F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107

F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958

F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220

F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]//
8.3e-18:353:65//Hs.60895:AA428463

F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357

F-MAMMA1002618

F-MAMMA1002619

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90
//Hs.47344:AF041449

F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300

F-MAMMA1002625

F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0507//1.1e-35:355:76//Hs.158241:AB007976

F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-
05:439:61//Hs.91400:AB006626

F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733
 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190
 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:AI393335
 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:AI005489
 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64/
 /Hs.8262:U36336
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-0
 6:272:64//Hs.106070:U22398
 F-MAMMA1002673
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.
 2e-162:752:99//Hs.3363:D86987
 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915
 F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:AI220397
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81
 //Hs.22396:AF062085
 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:AI274697
 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, comp
 lete cds//1.1e-51:307:79//Hs.46328:D87942
 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041
 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692
 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165
 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC
 RIBONUCLEASE [Saccharomyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193
 502
 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853
 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312
 F-MAMMA1002748
 F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848

F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98/
/Hs.32168:AB007902
F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293
F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782
F-MAMMA1002769
F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M860
4 Met protein (M8604 Met) gene//7.6e-84:417:97//Hs.77705:U07563
F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988
F-MAMMA1002782
F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:AI380710
F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919
F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI378514
F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.
4e-57:286:88//Hs.15731:AB011135
F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:7
2//Hs.22271:D26067
F-MAMMA1002835
F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE C
HAIN 1 [Locusta migratoria]//7.7e-38:179:78//Hs.141344:H29951
F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590
F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4
e-137:635:99//Hs.7531:AB018353
F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:3
29:58//Hs.107747:AI357868
F-MAMMA1002858
F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643
F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//
Hs.83987:U09284
F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423

F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI183632
 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete
 cds//3.8e-30:680:61//Hs.129732:D45027
 F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:6
 0//Hs.19944:U04270
 F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657
 F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666
 F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265
 F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.0
 0053:382:57//Hs.61796:U85658
 F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952
 F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125
 F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730
 F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapien
 s] //7.9e-103:485:99//Hs.102928:AI346344
 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.
 6e-194:910:98//Hs.31720:AB014598
 F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI423389
 F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:AI313418
 F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs
 .54697:AB007884
 F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400
 F-MAMMA1002972
 F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932
 F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944
 F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095645
 F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//
 3.9e-22:185:83//Hs.62192:J02931
 F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA

0501//1.0e-16:343:61//Hs.159897:AB007970
 F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979
 F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2
 e-51:620:69//Hs.75258:AF054174
 F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347:58//Hs
 .74061:X59372
 F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062
 F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:AI374951
 F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137
 F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549
 F-MAMMA1003035
 F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391
 F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-9
 3:339:85//Hs.5247:AF029750
 F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639
 F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.el
 egans//1.0:209:60//Hs.99491:Y12336
 F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742
 F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518
 F-MAMMA1003056
 F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.
 musculus] //1.3e-88:334:97//Hs.96500:AI206781
 F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI022618
 F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5
 e-51:329:71//Hs.75154:AB014531
 F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA,
 complete cds//8.5e-44:288:88//Hs.81008:AF043045
 F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:21
 3:60//Hs.42945:Y08136

F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200
:64//Hs.32950:X82634

F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete
cds//5.4e-27:421:66//Hs.5394:AF105424

F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786

F-MAMMA1003140

F-MAMMA1003146//Homo sapiens mRNA for GALT3 protein//7.2e-82:397:97//Hs.
151344:Y15062

F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.0
0019:297:61//Hs.108945:AB011087

F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:48
7:65//Hs.3847:U59632

F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//H
s.79706:U53204

F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:9
2//Hs.82510:D31886

F-NT2RM1000032

F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:
81//Hs.78442:D83782

F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5
e-108:542:95//Hs.60103:AB014590

F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//H
s.79706:U53204

F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:3
53:96//Hs.154980:AA948067

F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA,
complete cds//0.029:281:59//Hs.46465:U45285

F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210

F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:

97//Hs.3439:AC004472

F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.

8e-116:550:97//Hs.65238:AB014561

F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190
:63//Hs.431:L13689

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00
086:126:70//Hs.92693:AF007155

F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054

F-NT2RM1000127

F-NT2RM1000131

F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subun
it mRNA, nuclear gene encoding mitochondrial protein, complete cds//3.7e
-92:448:97//Hs.49767:AF044959

F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, compl
ete cds//1.0:546:58//Hs.110099:AB010419

F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00
081:126:70//Hs.92693:AF007155

F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:AI424382

F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.
87:454:59//Hs.47061:AF045458

F-NT2RM1000242

F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NA
P1) mRNA, complete cds//0.97:135:66//Hs.27910:AF049105

F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190

F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248
:69//Hs.1674:M90516

F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens
]//2.9e-98:530:93//Hs.104650:AI037879

F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:

80//Hs.23106:D50920

F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047

F-NT2RM1000272

F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D
[Bos taurus]//1.3e-21:308:73//Hs.15071:AA781144

F-NT2RM1000300

F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708
:92//Hs.5719:D63880

F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e
-35:182:99//Hs.9837:D79205

F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976

F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798

F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:3
87:95//Hs.108619:W28608

F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691

F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.
sapiens]//7.4e-91:481:95//Hs.163707:AA137181

F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X8050
7

F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353

F-NT2RM1000399

F-NT2RM1000421

F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, c
omplete cds//1.2e-85:418:97//Hs.20815:AF084928

F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]//1.
6e-38:201:97//Hs.106262:AI052382

F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284660

F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847

F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI359957

F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.79706:U53204

F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:26:61//Hs.17931:AB006625

F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]//6.2e-51:254:98//Hs.132096:AA314601

F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds//8.5e-55:276:97//Hs.19122:AF038957

F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.113936:AB005297

F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI188279

F-NT2RM1000672

F-NT2RM1000691//Homa sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:582:98//Hs.146282:AB015348

F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101

F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-66:435:85//Hs.5038:AJ004832

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6e-127:690:92//Hs.147946:AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:524:83//Hs.112360:AF027208

F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465

F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63//Hs.150390:AB007885

F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.053:271:60//Hs.139745:U39067

F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9e-20:128:94//Hs.23094:M19503

F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845
F-NT2RM1000800
F-NT2RM1000802
F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:4
90:84//Hs.112360:AF027208
F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI359957
F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:2
83:58//Hs.2314:X15422
F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//
Hs.1376:U26726
F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8
e-06:384:59//Hs.90314:L05148
F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partia
l//3.0e-149:726:97//Hs.99423:AJ010840
F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643
F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//5.3e-5
4:277:96//Hs.11125:AI015619
F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239
F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730)
containing the hFEN1 gene//4.0e-155:750:97//Hs.132898:AC004770
F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, comple
te cds//8.8e-158:762:97//Hs.26285:AF082516
F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.
3e-19:310:67//Hs.65238:AB014561
F-NT2RM1000894
F-NT2RM1000898
F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI268701
F-NT2RM1000924//HOMEBOX PROTEIN HOX-A5//0.00051:458:59//Hs.37034:M26679
F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.0

84:386:58//Hs.101474:AB018350
 F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//
 Hs.83419:D87440
 F-NT2RM1000978
 F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA,
 complete cds//1.3e-161:760:98//Hs.58488:U97067
 F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI025200
 F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395
 F-NT2RM1001044//ESTs, Weakly similar to C43E11.9 [C.elegans]//3.0e-98:49
 1:96//Hs.102173:AA045270
 F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533:57//H
 s.79706:U53204
 F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:AI380703
 F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:5
 86:56//Hs.62354:M83822
 F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)
 //0.0019:294:64//Hs.30223:X90846
 F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198
 F-NT2RM1001085
 F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.74107:
 X59244
 F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:AI343331
 F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:U10564
 F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495
 F-NT2RM1001115
 F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074
 F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113
 F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:640:59
 //Hs.148027:X63563

F-NT2RM2000030

F-NT2RM2000032//ESTs//7.1e-18:138:68//Hs.114031:AA700958

F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:AI286243

F-NT2RM2000092

F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085

F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428

F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-4
6:287:88//Hs.77271:X07767

F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//3.0e-139:566:97//Hs.18953:AF067223

F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999

F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans] //3.6e-93:489
:95//Hs.143499:R72672

F-nnnnnnnnnnnnn//ESTs//1.0e-70:269:97//Hs.156175:AI334328

F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.
0e-129:615:98//Hs.111862:AB011162

F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520

F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500

F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981

F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54434:U5
1127

F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.
8e-176:805:99//Hs.129952:AB011132

F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543

F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA
, partial cds//3.7e-96:599:86//Hs.75871:U48251

F-NT2RM2000371

F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866

F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L13698

F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.28757:U
81006

F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582

F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053

F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, s
erotonin), member 4//1.5e-06:260:61//Hs.553:L05568

F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:AI097379

F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:AI281807

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4
e-16:386:63//Hs.8309:AB018290

F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, comp
lete cds//0.99:272:61//Hs.76669:U08021

F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds/
/1.6e-172:824:97//Hs.4812:AF061243

F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313:6
0//Hs.129725:AF047487

F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]
//2.7e-41:231:94//Hs.7049:AI141736

F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220

F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF032108

F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.
89631:U48508

F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128

F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITO
CHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993

F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.
8e-175:820:98//Hs.3363:D86987

F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220

F-NT2RM2000594

F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.0
17:253:65//Hs.102402:AF040963

F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313

F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548

F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.0
24:326:59//Hs.6150:AB011093

F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258

F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0
e-143:664:98//Hs.19542:AB018272

F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4
e-139:664:98//Hs.7278:AB014558

F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702

F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4
e-169:518:99//Hs.115763:AB014576

F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:AI337371

F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, com
plete cds//6.7e-86:746:74//Hs.5321:AF006083

F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:6
4//Hs.7938:D86984

F-NT2RM2000718//Homa sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:
594:98//Hs.136058:AB015342

F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107
:X59244

F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE
IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:9
1//Hs.161551:W24286

F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-8
2:640:81//Hs.5247:AF029750

F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//

Hs.105919:AB002338

F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701

F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2
.8e-185:847:99//Hs.137580:AB015046

F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanog
aster] //6.2e-94:441:99//Hs.59075:AI023761

F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//
Hs.84753:D87433

F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831

F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cer
evisiae] //2.9e-48:282:93//Hs.17035:AI080471

F-NT2RM2001065

F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding mo
tif, complete cds//1.7e-08:449:62//Hs.75111:D87258

F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear prot
ein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153

F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190

F-NT2RM2001141

F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042

F-NT2RM2001177

F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans] //2.4e-23:14
9:93//Hs.10618:AI288739

F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959

F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:
69//Hs.155291:D13630

F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.
97:165:64//Hs.24279:AB018349

F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766

F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:

64//Hs.75889:U65928

F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066
:321:61//Hs.132206:AF039694

F-NT2RM2001256

F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845

F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:
182:65//Hs.75221:AF001601

F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615

F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.eleg
ans]//5.2e-30:277:77//Hs.25347:AI138605

F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0
.031:245:62//Hs.26915:AB008567

F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706

F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905

F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61/
/Hs.82925:U70322

F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:
U68382

F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378

F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e
-97:453:99//Hs.155218:AJ007509

F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X
57303

F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328
:60//Hs.68900:AF016903

F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969

F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459

F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262

F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein aut

oantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800
 F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:5
 7:89//Hs.114722:AA448077
 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65/
 /Hs.32168:AB007902
 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729
 F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//
 Hs.76272:S66431
 F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61
 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
 F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918
 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.
 0e-154:740:98//Hs.15832:AB014518
 F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952
 F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [B
 os taurus]//3.5e-13:94:92//Hs.22142:AA814725
 F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61
 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
 F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301
 F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (
 IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195
 F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH
 6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907
 F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1
 e-25:352:70//Hs.101414:AB011129
 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356
 F-NT2RM2001675
 F-NT2RM2001681//ESTs//0.16:197:63//Hs.20585:R10305

F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211
 F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216
 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//
 5.8e-16:144:84//Hs.14671:T79937
 F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415
 F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817
 F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826
 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788
 F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650
 F-NT2RM2001718
 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//
 Hs.12457:AF052123
 F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0
 e-112:530:98//Hs.129937:AB007931
 F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.
 95:269:58//Hs.129952:AB011132
 F-NT2RM2001743
 F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:A
 B011399
 F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61
 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
 F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742
 F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:
 X78933
 F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698
 F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595
 F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730)
 containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770

F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763

F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175

F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195

F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341

F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068

F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759

F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080

F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567

F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741

F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:AB014610

F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:AB007931

F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:U52840

F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688

F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//
2.2e-139:653:98//Hs.21811:AF091080
F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392
F-NT2RM2001982
F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds
//1.2e-21:123:98//Hs.6454:AF089816
F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.1041
35:AJ006778
F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538
F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:2
71:60//Hs.63888:AA203398
F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5
e-37:509:65//Hs.6214:AB018274
F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:4
29:58//Hs.79090:D89729
F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822
:73//Hs.1674:M90516
F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427
F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154
F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377
F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.896
31:U48508
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partia
l//2.5e-165:776:98//Hs.99423:AJ010840
F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (G
AC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435
F-NT2RM2002128
F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274
F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, c

omplete cds//1.4e-144:800:92//Hs.20815:AF084928
 F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7
 e-165:787:97//Hs.11147:AB007936
 F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palm
 aris et plantaris)//0.064:291:61//Hs.99936:X14487
 F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59
 //Hs.148027:X63563
 F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074
 F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464
 F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674
 F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511
 F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is rel
 ated to human RNA helicase A. [H.sapiens]//1.6e-30:369:70//Hs.114623:AI2
 04280
 F-NT2RM4000086
 F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (Z
 NF210) mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865
 F-NT2RM4000139
 F-NT2RM4000155
 F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632
 F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, c
 omplete cds//9.8e-30:676:61//Hs.159228:AF041853
 F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044
 F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190
 F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744
 F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
 RY !!!! [H.sapiens]//0.13:322:61//Hs.145088:AI221147
 F-NT2RM4000200
 F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.002

7:424:60//Hs.91400:AB006626
 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.
 4e-184:856:98//Hs.111138:AB018255
 F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013
 :358:60//Hs.75055:M93651
 F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.
 65:572:60//Hs.47061:AF045458
 F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582
 F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439
 F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyce
 s pombe]//1.1e-16:112:92//Hs.93841:AA442297
 F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, comp
 lete cds//1.8e-48:229:83//Hs.46328:D87942
 F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, comp
 lete cds//2.5e-154:609:93//Hs.31305:M99438
 F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds/
 /0.070:460:59//Hs.5372:AB000712
 F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707
 F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces cer
 evisiae]//2.7e-83:432:95//Hs.12796:W27884
 F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:
 68//Hs.155291:D13630
 F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.melanog
 aster]//0.0078:55:92//Hs.59075:AI023761
 F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425
 F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3
 e-135:628:99//Hs.8152:AB014542
 F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745
 F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25.

Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022718

F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029

F-NT2RM4000414//Homo sapiens XYL B mRNA for xylulokinase, complete cds//4.9e-17:114:94//Hs.137580:AB015046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs.154872:AB011166

F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543:58//Hs.2175:M59820

F-NT2RM4000457

F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:63//Hs.66369:U95040

F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:AI280004

F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632

F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915

F-NT2RM4000514

F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409

F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:AI221305

F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus] //1.8e-153:756:96//Hs.125870:AI364967

F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78987

F-NT2RM4000534

F-NT2RM4000585

F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:62//Hs.7764:AB007938

F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN CO
2F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:532:96//Hs.60
92:T75227

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:6
8//Hs.40100:AB002390

F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068

F-NT2RM4000616

F-NT2RM4000674

F-NT2RM4000689

F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA,
partial cds//3.5e-91:744:77//Hs.42400:AF022789

F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PR
ECURSOR [Mus musculus]//2.6e-163:771:97//Hs.6823:W18181

F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2
e-159:743:98//Hs.137168:AB018303

F-NT2RM4000741

F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus
musculus]//1.1e-75:388:96//Hs.112361:R99396

F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815

F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731

F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.
8e-173:810:98//Hs.18586:AB007920

F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186

F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:
98//Hs.25817:AC005306

F-NT2RM4000795//ESTs, Highly similar to LIVER CARBOXYLESTERASE PRECURSO

R [Homo sapiens] //6.7e-19:160:80//Hs.124902:AI337820
F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292:62
//Hs.124212:M64676
F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301
F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subu
nit (SNAP190) mRNA, complete cds//0.052:238:64//Hs.113265:AF032387
F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568
F-NT2RM4000833
F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//
Hs.7841:AB002322
F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934
F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN
SUBSTRATE 2 [Homo sapiens] //4.4e-29:164:95//Hs.115095:AI392943
F-NT2RM4000887
F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyr
ophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011004
F-NT2RM4000950
F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546
F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77
//Hs.7289:AB007875
F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs.2481:X
78926
F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6
e-171:803:98//Hs.19542:AB018272
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1
e-126:584:99//Hs.15711:AB014539
F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.
8e-05:469:58//Hs.5333:AB018254
F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus] //7

.0e-56:340:92//Hs.87310:AI247543
 F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM
 " PRECURSOR//0.79:142:69//Hs.77424:M63835
 F-NT2RM4001084
 F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62
 //Hs.108947:D30758
 F-NT2RM4001116
 F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:
 61//Hs.134989:L12701
 F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730
 F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI004145
 F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351
 F-NT2RM4001187
 F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220
 F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:
 X78933
 F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete c
 ds//1.4e-153:707:99//Hs.14934:AF004828
 F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEI
 N ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]//0.19:291:62//Hs.31
 582:AA877205
 F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, c
 omplete cds//7.0e-63:715:70//Hs.104925:AF059611
 F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C
 .elegans]//1.1e-67:208:96//Hs.26676:AA033997
 F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.
 0019:435:59//Hs.6360:AB007950
 F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:
 59//Hs.26971:AC003003

F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-7
9:474:89//Hs.32971:Z46973

F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335

F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:
66//Hs.87435:D89016

F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI418988

F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEI
N IN PMI40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0096:284
:58//Hs.120997:R56714

F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat reg
ion of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-52:252:100//Hs
.15301:AA167818

F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656

F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-
169:790:98//Hs.5151:AF098799

F-NT2RM4001384

F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575

F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64/
/Hs.105052:AB000520

F-NT2RM4001412

F-NT2RM4001414//ESTs, Moderately similar to F18547_1 [H.sapiens]//5.2e-1
8:133:87//Hs.28209:AI073817

F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:7
0//Hs.154326:D42087

F-NT2RM4001444

F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914

F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sa
piens]//1.1e-71:313:99//Hs.163754:AA587784

F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585

F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619

F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae] //1.3e-114:536:99//Hs.88820:AA456247

F-NT2RM4001557

F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487

F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453

F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859

F-NT2RM4001582

F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566

F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:AB011094

F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus] //2.3e-72:387:95//Hs.114722:AA448077

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:AB018334

F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans] //8.6e-05:91:79//Hs.24647:W19739

F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens] //0.0042:153:68//Hs.114832:AI147946

F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320

F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323

F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638

F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384

F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957

F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905

F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903

F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318

F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306

F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus] //2.0e-27:205:83//Hs.110601:AA206719

F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630

F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:AB018270

F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans] //3.1e-71:376:95//Hs.108396:AA160677

F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NA P1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105

F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547

F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712

F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens] //2.3e-40:252:90//Hs.119294:AI379442

F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687

F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824

F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204

F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814

F-NT2RM4001856

F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator

T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250

F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.

3e-150:704:98//Hs.61628:Y17711

F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:6

6//Hs.7938:D86984

F-NT2RM4001880

F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:AI312633

F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, part

ial cds//0.98:359:57//Hs.155356:AJ224875

F-NT2RM4001938

F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-1

72:808:98//Hs.118631:AF098162

F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:8

3//Hs.154326:D42087

F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel.

[H.sapiens]//1.8e-65:337:96//Hs.130135:AA905493

F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862

F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.

2e-63:527:76//Hs.159277:AB018341

F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082

F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.7

3:181:65//Hs.11147:AB007936

F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271

F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601

F-NT2RM4002034

F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048

F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912

F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540

F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//7.0e-94:396:94//Hs.59346:AI126802

F-NT2RM4002063

F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309

F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040

F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302

F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.122967:AF059569

F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products} //9.2e-34:532:65//Hs.146459:X66975

F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743

F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542

F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877

F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158

F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650:AI037879

F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535

F-NT2RM4002174

F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L2199

8

F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//
7.3e-11:454:60//Hs.32981:U38276

F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454

F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.5
2:313:61//Hs.118087:AB011182

F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUN
D [*Drosophila melanogaster*]//8.4e-125:588:98//Hs.23900:U82984

F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966

F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764

F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57
//Hs.77783:AF014118

F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180

F-NT2RM4002281

F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979

F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:
72//Hs.31463:D87457

F-NT2RM4002301

F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331

F-NT2RM4002339

F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454

F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.
1e-151:708:98//Hs.26163:AB014549

F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0
040:303:63//Hs.23741:AB018263

F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293

F-NT2RM4002390

F-NT2RM4002398

F-NT2RM4002409

F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C .elegans] //1.1e-55:282:96//Hs.26676:AA033997

F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151

F-NT2RM4002452

F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783

F-NT2RM4002460//EST//1.0:142:65//Hs.145370:AI252780

F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777:98//Hs.8765:AF083255

F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781:AB014591

F-NT2RM4002493

F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347

F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219

F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968:U02020

F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075

F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100:70//Hs.159483:AF054176

F-NT2RM4002558//Homo sapiens amphipysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004

F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273

F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans] //3.3e-88:484:93//Hs.105837:AA536054

F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylgl

alactosaminyltransferase [H.sapiens]//0.059:121:70//Hs.155413:AA429394
 F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151
 F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275
 F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402
 F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587
 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449
 F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907
 F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647
 F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834
 F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924
 F-NT2RP1000111
 F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699
 F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025
 F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:382:94//Hs.127842:W38901
 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792
 F-NT2RP1000170//EST//0.68:130:63//Hs.146994:AI184430
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535
 F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499
 F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703
 F-NT2RP1000243

F-NT2RP1000259

F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.4214:AF067730

F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661

F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551.

F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231

F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204

F-NT2RP1000357

F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807

F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864:AB014538

F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594

F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031

F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862:AB011159

F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//7.3e-177:857:97//Hs.6823:W18181

F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:60//Hs.89230:AF031815

F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603

F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862

F-NT2RP1000460

F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, gen

omic sequence//3.7e-134:665:96//Hs.143187:AC002985
 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.159154:U47634
 F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102
 F-NT2RP1000493
 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977
 F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992
 F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.104105:AF017418
 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213
 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770
 F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475
 F-NT2RP1000630
 F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U24576
 F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553
 F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI141736
 F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148
 F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.

0e-33:278:78//Hs.58167:D30612

F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens] //6.2e-40:297:84//Hs.18122:AI338045

F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644

F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434

F-NT2RP1000746

F-NT2RP1000767

F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023

F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401

F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//2.7e-23:147:91//Hs.102336:Z83838

F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:96//Hs.18953:AF067223

F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903

F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990

F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838

F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875

F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023

F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094

F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683

F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:AI248847

F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm04e9 [C.elegans] //2.2e-27:159:94//Hs.122153:AA780270

F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U
76248

F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400

F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbCH5B (UBCH5B) mR
NA, complete cds//2.7e-26:185:87//Hs.108332:U39317

F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.1
54276:AB002803

F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847

F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M1788
5

F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858

F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//H
s.82837:L13435

F-NT2RP1001011

F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163

F-NT2RP1001014

F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M6
1764

F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901

F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531

F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cd
s//0.57:215:64//Hs.14845:AF032886

F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEE
SB82F [C.elegans]//1.4e-65:293:95//Hs.32751:H38087

F-NT2RP1001173

F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1
e-26:259:74//Hs.75258:AF054174

F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524

F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150
F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523
F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094
F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231
F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724
F-NT2RP1001294
F-NT2RP1001302
F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341
F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815
F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770
F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//6.8e-101:480:94//Hs.75017:AA166853
F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859
F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673
F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081
F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700
F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700
F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149
F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104
F-NT2RP1001466
F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742
F-NT2RP1001482

F-NT2RP1001494

F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400

F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:
254:64//Hs.75814:AB000277

F-NT2RP1001569

F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds
//2.5e-41:496:74//Hs.12956:U90913

F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420

F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//
4.7e-137:685:96//Hs.93677:AF091081

F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C.elegans]//8.2e-47:30
0:89//Hs.6473:AA853955

F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:6
8//Hs.40100:AB002390

F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:6
6//Hs.70617:D31763

F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HO
MOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359

F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1
e-78:383:97//Hs.8309:AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homol
og (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749

F-NT2RP2000054//HOMEBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:
L20433

F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase
epsilon//1.2e-27:146:100//Hs.155991:X54134

F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25.
Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (1

ymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609

F-NT2RP2000076//H.sapiens mRNA for TFIIA//0.00023:356:62//Hs.121686:D14887

F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078

F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338

F-NT2RP2000091

F-NT2RP2000097

F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963

F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390

F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-15:551:97//Hs.17706:AB018356

F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670

F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177

F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195

F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475

F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910

F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291

F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190
F-NT2RP2000173
F-NT2RP2000175
F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713
F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:AI148761
F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050
F-NT2RP2000208
F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:243:61//Hs.143641:AB009462
F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990
F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342:59//Hs.8546:U97669
F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//Hs.47822:AB002378
F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719
F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like) //0.51:227:60//Hs.30223:X90846
F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691
F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011
F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599
F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910
F-NT2RP2000288
F-NT2RP2000289
F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744:70//Hs.37138:U35376
F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:AI123467
F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA

, complete cds//4.3e-13:140:80//Hs.58218:U82381
 F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:AI417006
 F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:AI332905
 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66
 //Hs.101642:X60673
 F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:1
 26:69//Hs.153706:AF026547
 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA,
 complete cds//1.2e-130:627:97//Hs.76556:U83981
 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.5
 6:464:57//Hs.12259:AB014530
 F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67
 :375:93//Hs.808:L28010
 F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapie
 ns] //3.9e-75:413:92//Hs.36779:AA626790
 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA,
 complete cds//6.7e-128:609:96//Hs.5819:AF102265
 F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381
 F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:AI393918
 F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.154655:
 Z68747
 F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293
 F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702
 F-NT2RP2000510
 F-NT2RP2000516
 F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING P
 ROTEIN [Rattus norvegicus] //3.2e-15:167:75//Hs.10984:AA806768
 F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6

e-38:196:98//Hs.14409:AB011144
 F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0:242:57//Hs.114001:Z20656
 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:97//Hs.7314:AB014514
 F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174
 F-NT2RP2000656
 F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602
 F-NT2RP2000668
 F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453
 F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233:78//Hs.114905:AA088442
 F-NT2RP2000710
 F-NT2RP2000715
 F-NT2RP2000731
 F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242
 F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:445:89//Hs.21421:AA911739
 F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880
 F-NT2RP2000814
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182
 F-NT2RP2000819
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, compl

ete cds//9.5e-29:167:94//Hs.75794:U80811
 F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:AI336850
 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2
 F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe] //6.4e-34:207:92//Hs.1
 35235:AI081880
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.
 7e-142:732:94//Hs.3615:AB018284
 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase
 kinase 5 [H.sapiens] //0.50:189:65//Hs.46146:AA418097
 F-NT2RP2000931//MATRIN 3//1.1e-130:610:98//Hs.78825:AB018266
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:9
 7//Hs.15144:AC005014
 F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.
 9e-113:533:98//Hs.19822:AB018298
 F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494
 F-NT2RP2000970
 F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN
 SIS2-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae] //7.3e-76:385:96//
 Hs.21875:AA243700
 F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944
 F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292
 F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
 0488//1.0e-145:696:97//Hs.67619:AB007957
 F-NT2RP2001065
 F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//H
 s.3989:AB002313
 F-NT2RP2001081

F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:AI356560

F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219

F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191

F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:201:91//Hs.118470:AI336362

F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582

F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:AI091361

F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247:AB007949

F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011

F-NT2RP2001196

F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598

F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053

F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//Hs.69740:U09367

F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813

F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353

F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277

F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:76//Hs.75848:U39412

F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287

F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387

F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs.76090:M80783

F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522

F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883
F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans] //1.8e-72:41
8:91//Hs.107039:W27244
F-NT2RP2001378
F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377558
F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155),
complete sequence//0.28:225:62//Hs.159402:AC005609
F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767
F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088
F-NT2RP2001420
F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]
//0.030:443:59//Hs.140506:AA308018
F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875
F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966
F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase acti
vation protein, eta polypeptide//9.8e-56:603:72//Hs.75544:Z82248
F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218
F-NT2RP2001449
F-NT2RP2001450
F-NT2RP2001467
F-NT2RP2001506
F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans] //3.2e-83:409
:98//Hs.156161:AI333779
F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARAL
AR1//6.4e-138:657:97//Hs.4277:Y14494
F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134
F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3
(XRCC3) mRNA, complete cds//5.2e-105:384:94//Hs.99742:AF035586
F-NT2RP2001560

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0488//1.4e-124:590:98//Hs.67619:AB007957

F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:5
21:60//Hs.75936:U28389

F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876

F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//
Hs.82201:M55268

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3
e-138:647:98//Hs.27197:AB018340

F-NT2RP2001613

F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229

F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA,
complete cds//4.9e-124:604:96//Hs.58488:U97067

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD
subunit brain-specific isoform mRNA, complete cds//1.3e-145:687:97//Hs.1
59558:AF058718

F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328

F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936

F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.0
28:285:63//Hs.6162:AB018314

F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.
7e-34:328:76//Hs.27621:U52840

F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091

F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.mu
sculus]//1.0:173:62//Hs.107361:AI197870

F-NT2RP2001721

F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:
57//Hs.8114:AF022991

F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate sy

nthease, dimethylallyltranstransferase, geranyltranstransferase)//1.2e-
 19:151:86//Hs.77393:D14697
 F-NT2RP2001762//Homo sapiens exonuclease 1a (EX01a) mRNA, complete cds//
 5.2e-34:191:96//Hs.47504:AF091754
 F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180
 F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250
 F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497
 :Y16610
 F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0
 .0013:174:62//Hs.9443:AF027219
 F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.7636
 4:Y14768
 F-NT2RP2001883
 F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURS
 OR//3.0e-113:633:90//Hs.142189:M74161
 F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650
 F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]
 //0.37:263:62//Hs.106377:H29757
 F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754
 F-NT2RP2001936
 F-NT2RP2001943
 F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
 F-NT2RP2001947
 F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489
 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//H
 s.155174:AB007892
 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4
 e-05:235:62//Hs.129943:AB011117
 F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196

F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:AB018299

F-NT2RP2002032

F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543

F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336

F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509

F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198

F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284

F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66//Hs.44553:AF055634

F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241

F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183

F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014

F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156

F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:97//Hs.155218:AJ007509

F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.122755:AF032986

F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286

F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363

F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112

F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314

F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:C06057

F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7

e-37:194:97//Hs.91728:M58460

F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein
PIASx-alpha mRNA, complete cds//6.8e-15:228:67//Hs.111323:AF077954

F-NT2RP2002208

F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628

F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318

F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264
:U70439

F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.7
9:264:59//Hs.129748:AB011099

F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cd
s//2.1e-51:315:89//Hs.150595:AF005418

F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//
Hs.92137:M19720

F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-3
1:206:88//Hs.4029:Z78373

F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079

F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA,
partial cds//5.0e-95:467:96//Hs.24812:AF069532

F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445

F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA
, complete cds//1.3e-124:640:95//Hs.31034:AB015594

F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60/
/Hs.75516:X54637

F-NT2RP2002373

F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant m
RNA, complete cds//3.1e-139:673:97//Hs.109051:AF038958

F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U
79289

F-NT2RP2002408//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74
095:L20433

F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098

F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326

F-NT2RP2002442//ESTs, Weakly similar to similar to molybdoterin biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265

F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045

F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929

F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs.125856:AB005289

F-NT2RP2002498

F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044

F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255:AB018334

F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212

F-NT2RP2002537

F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096

F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979

F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277:AB018341

F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309

F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503

F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334:U02082

F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805

F-NT2RP2002621

F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs.155302:U57317

F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493

F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK 757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385

F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336:AB014572

F-NT2RP2002727

F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217

F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297

F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016

F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329

F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709

F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705

F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204

F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407

F-NT2RP2002800

F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763

F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142

F-NT2RP2002862

F-NT2RP2002880

F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0
:237:62//Hs.106487:AB014573

F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606

F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.116674:AF038392

F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:15
8:65//Hs.108447:AJ000517

F-NT2RP2002939

F-NT2RP2002954

F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds//6.4e-21:135:91//Hs.108332:U39317

F-NT2RP2002979

F-NT2RP2002980

F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.122967:AF059569

F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:AI004740

F-NT2RP2002993

F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs
.155464:AF088219

F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741

F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019

F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190

F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs
.153704:U11050

F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633

F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379

F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161

F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544
F-NT2RP2003137
F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.4
0:227:61//Hs.105958:AB014520
F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete c
ds//5.7e-113:581:93//Hs.9736:D67025
F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:AI424170
F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944
F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:
79//Hs.153014:AB002353
F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N91123
F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:AI393223
F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594
F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794
F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947
F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phos
phate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//Hs.108966:U486
96
F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear prot
ein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153
F-NT2RP2003265
F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]
//5.8e-57:313:93//Hs.109966:C06057
F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9
e-147:714:96//Hs.154919:AB014525
F-NT2RP2003280
F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.
0097:243:65//Hs.21862:AB011159
F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:AI269334

F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//2.0e-86:416:97//Hs.7943:AB006572

F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312

F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752

F-NT2RP2003308

F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN CO 2F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092:T75227

F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:AI346765

F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963

F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108

F-NT2RP2003391

F-NT2RP2003393

F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023

F-NT2RP2003401

F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//3.7e-33:303:77//Hs.14038:R06800

F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893

F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273:61//Hs.159360:L22647

F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770

F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106

F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136

F-NT2RP2003506

F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.1071
64:M96803

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:9
4//Hs.78482:Y16270

F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian
sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783

F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112
180:AF039019

F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765

F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010

F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513

F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein aut
oantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3
e-114:541:98//Hs.129937:AB007931

F-NT2RP2003581//EST//1.0:59:76//Hs.158575:AI368947

F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.eleg
ans]//1.3e-63:224:95//Hs.34627:AA126463

F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA,
complete cds//1.7e-124:585:98//Hs.58488:U97067

F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166

F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M972
52

F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HP
X42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006

F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:AI032875

F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247

F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61

//Hs.18366:L09561

F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271

F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097

F-NT2RP2003713

F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180

F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879

F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme Ubch5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U39318

F-NT2RP2003751

F-NT2RP2003760

F-NT2RP2003764

F-NT2RP2003769

F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677

F-NT2RP2003777

F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:356:92//Hs.16131:AA568689

F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955

F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742

F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368

F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425

F-NT2RP2003859

F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780

F-NT2RP2003885

F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emericella nidulans]//2.2e-113:632:92//Hs.50072:AI378221

F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H
 .sapiens] //1.0:146:67//Hs.156920:AA489296

F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease,
 complete cds//6.8e-30:165:96//Hs.35086:AB014458

F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.
 9e-116:610:94//Hs.7302:AB007916

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2
 e-161:783:96//Hs.7316:AB018347

F-NT2RP2003984

F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036

F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124
 :AF019369

F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo
 sapiens] //7.0e-104:556:93//Hs.111081:AI380378

F-NT2RP2004014

F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:8
 0//Hs.10116:AC004780

F-NT2RP2004042

F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete
 cds//0.80:292:61//Hs.1147:AF011573

F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942

F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2)
 mRNA, complete cds//0.15:199:60//Hs.104315:AF054828

F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:
 AJ007292

F-NT2RP2004142

F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872

F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.6
 9:176:63//Hs.78353:U88666

F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966
 F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501
 F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapie
 ns] //1.7e-16:276:67//Hs.36779:AA626790
 F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete
 cds//1.0:124:69//Hs.155302:U57317
 F-NT2RP2004196
 F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756
 F-NT2RP2004226//ESTs, Weakly similar to teg292 protein [M.musculus] //1.8
 e-80:386:98//Hs.68791:AA527270
 F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756
 F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680
 F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536
 F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:5
 9//Hs.129725:AF047487
 F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.eleg
 ans] //8.2e-51:474:74//Hs.108990:N25951
 F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//
 Hs.112432:AC005263
 F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERAS
 E BETA 3//0.35:157:67//Hs.37121:Z37544
 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete c
 ds//1.5e-151:735:97//Hs.61152:AF000416
 F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735
 F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510
 F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632
 F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202
 F-NT2RP2004365
 F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript

//0.60:295:57//Hs.39163:AF000986

F-NT2RP2004373

F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F0
9G8.3 IN CHROMOSOME III [Caenorhabditis elegans] //3.3e-97:477:98//Hs.304
90:AA146916

F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588

F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:
95//Hs.152759:AC005164

F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans] //1.2e-92:51
9:91//Hs.13275:AI341468

F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367

F-NT2RP2004412

F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944

F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687

F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TAS
K) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823

F-NT2RP2004490

F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203

F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA,
complete cds//1.3e-29:270:79//Hs.73614:U83460

F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6
e-139:687:96//Hs.129908:AB011163

F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891

F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-0
6:291:61//Hs.132206:AF039694

F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs
.155464:AF088219

F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.
98:136:64//Hs.28020:AB018309

F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.
0:104:68//Hs.125729:N99898

F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.
.24756:U43895

F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENT
RY !!!! [H.sapiens]//3.0e-59:273:93//Hs.12845:N28835

F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496
:98//Hs.5198:AJ006291

F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2
e-155:728:98//Hs.29956:AB007929

F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839

F-NT2RP2004681

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1
e-61:327:94//Hs.154919:AB014525

F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942

F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.
1e-118:582:96//Hs.4236:AB007947

F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242

F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183

F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE
PAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504

F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA
, complete cds//0.025:547:57//Hs.107474:AF045451

F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete
cds//0.99:121:64//Hs.2864:L40157

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta s
ubunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF058953

F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043
 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:AF054179
 F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161
 F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258
 F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111
 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144
 F-NT2RP2004936
 F-NT2RP2004959
 F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763
 F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478
 F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735
 F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927
 F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.41723:U37426
 F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478
 F-NT2RP2004999
 F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//Hs.124161:AF065164
 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:AB014515
 F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141

F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600
F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433
F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067
F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035
F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612
F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:AF055917
F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838
F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616:AB014564
F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.100555:X98743
F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803
F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947
F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:AF045583
F-NT2RP2005147
F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582
F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:AI357868
F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218:AJ007509
F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159
F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189

F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783

F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U70439

F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341

F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.81452:AF030555

F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932

F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//Hs.27007:AF060219

F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590

F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833

F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:AB014576

F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.1569:U11701

F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.016:353:62//Hs.113265:AF032387

F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138

F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958

F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:489:96//Hs.107254:AC005943

F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122

F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.113252:U80761

F-NT2RP2005407

F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.2

8:338:57//Hs.6189:AB011133
 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068
 F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164
 F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE
 SUBUNIT B14.5B [Bos taurus]//8.5e-48:295:90//Hs.75017:AA166853
 F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243
 F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//0.032:1
 76:64//Hs.16:D10656
 F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AI378412
 F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.
 9e-48:432:77//Hs.15519:AB018315
 F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573
 F-NT2RP2005491
 F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:AI084164
 F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:6
 8//Hs.6833:AB002324
 F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete
 cds//1.6e-63:503:78//Hs.7688:M64930
 F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:13
 9:66//Hs.8546:U97669
 F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthe
 tase), regulatory (30.8kD)//1.0:291:59//Hs.89709:L35546
 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mR
 NA, complete cds//1.2e-82:444:92//Hs.119023:AF092563.
 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.
 2e-19:112:99//Hs.6232:AB018307
 F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1
 [H.sapiens]//3.5e-50:366:83//Hs.61833:AA036735
 F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e

-155:747:97//Hs.159597:AJ012449
 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.
 9e-131:618:98//Hs.62515:AB007963
 F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16
 C10.10 IN CHROMOSOME III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407
 F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822
 F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839
 F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436
 F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627
 F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071
 F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97
 //Hs.22396:AF062085
 F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702
 F-NT2RP2005635
 F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905
 F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145
 F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440
 F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.143065:M86
 917
 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-
 08:351:62//Hs.91400:AB006626
 F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239
 F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, co
 mplete cds//7.7e-96:462:98//Hs.25664:AF089814
 F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702
 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79
 217:M77836
 F-NT2RP2005694
 F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) m

RNA, complete cds//0.15:496:55//Hs.79326:L76703
 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:AB018342
 F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527
 F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//Hs.69740:U09367
 F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017
 F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191
 F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086
 F-NT2RP2005741//Homo sapiens chondroadherin gene, 5' flanking region and /0.80:362:58//Hs.97220:U96769
 F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//Hs.159651:AF068868
 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.26285:AF082516
 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853
 F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836
 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:Z50115
 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556
 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.34853:U28368
 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820
 F-NT2RP2005812

F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595
 F-NT2RP2005835
 F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA,
 complete cds//0.94:148:65//Hs.59829:AB014602
 F-NT2RP2005853
 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mR
 NA, partial cds//5.4e-176:829:98//Hs.50758:AF092564
 F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567
 F-NT2RP2005868
 F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, par
 tial cds//0.26:728:57//Hs.240:L16782
 F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943
 F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360
 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399
 F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//
 7.9e-90:326:98//Hs.156882:AA292186
 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770
 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339
 F-NT2RP2006023
 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382
 F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.5
 1:271:59//Hs.37035:U07664
 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093
 F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58
 //Hs.57652:D87469
 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416
 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970
 F-NT2RP2006100
 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135

F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349
F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240
F-NT2RP2006166
F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73/
/Hs.74368:X69910
F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5
e-114:567:96//Hs.109299:AB014554
F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.
0e-23:187:85//Hs.15519:AB018315
F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503
F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.15
3910:X96484
F-NT2RP2006237
F-NT2RP2006238
F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970
F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//
0.019:111:71//Hs.157199:X97630
F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding mo
tif, complete cds//2.4e-05:388:60//Hs.75111:D87258
F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:
598:97//Hs.3404:AF035262
F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.
musculus]//1.9e-29:151:100//Hs.36794:AI038407
F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371
F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:
70//Hs.87202:D82344
F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0
.11:43:100//Hs.6892:AF076974
F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1

e-05:233:65//Hs.37656:AB011174
F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501
F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341
F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734
F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934
F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509
F-NT2RP2006456
F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//1.1e-149:545:98//Hs.72160:AJ006266
F-NT2RP2006467
F-NT2RP2006472
F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048
F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134
F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966
F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U22029
F-NT2RP2006573
F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223
F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180
F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:AJ011972
F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:AF000560
F-NT2RP3000047
F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.37138:U35376
F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961

F-NT2RP3000068
F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769
F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353
:78//Hs.108287:L27670
F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//H
s.80741:X14608
F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140
F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595
F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:
438:100//Hs.8173:AC005189
F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9
e-182:849:98//Hs.13273:AB011164
F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1
e-20:133:94//Hs.23094:M19503
F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA
0492//6.6e-08:152:71//Hs.127338:AB007961
F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779
F-NT2RP3000207
F-NT2RP3000220
F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete
cds//6.6e-20:509:58//Hs.122967:AF059569
F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740
F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691
:86//Hs.75863:D86972
F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733
F-NT2RP3000252
F-NT2RP3000255
F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568
F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, comp

lete cds//1.7e-13:214:67//Hs.80261:L43821
 F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863
 F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153
 F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242
 F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189:65//Hs.46146:AA418097
 F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390
 F-NT2RP3000348
 F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754
 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:X60673
 F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921
 F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymanaea stagnalis]//4.0e-116:596:95//Hs.21094:AI337016
 F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639
 F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:AF071185
 F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610:65//Hs.23094:M19503
 F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948
 F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487
 F-NT2RP3000441
 F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562
 F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705

F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068
 F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822
 F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058
 F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667
 F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:
 63//Hs.79347:D86966
 F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308
 F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412
 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404
 F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723
 F-NT2RP3000578
 F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277
 F-NT2RP3000584
 F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904
 F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:5
 7//Hs.77234:AB001914
 F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811
 F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:35
 5:92//Hs.114622:AA693492
 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:5
 9//Hs.79170:D86980
 F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:AI421203
 F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683
 F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162
 F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333
 F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904
 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs
 .155464:AF088219

F-NT2RP3000661

F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.13063:AF017789

F-NT2RP3000685

F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001

F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884

F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854

F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:AI369426

F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765

F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245:91//Hs.2427:D89937

F-NT2RP3000815

F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132

F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700

F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN A P47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476

F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012

F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:X97630

F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520

F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs.155464:AF088219

F-NT2RP3000852

F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918

F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476

F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766:60//Hs.15432:U53445

F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60

//Hs.79706:U53204

F-NT2RP3000875

F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101

F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374

F-NT2RP3000917

F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277

F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X844
07

F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:AI204212

F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411

F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198

F-NT2RP3001007

F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen a
lpha chain 1(V) chain [C.elegans]//2.9e-121:588:98//Hs.128781:AA160707

F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sa
piens]//9.8e-54:282:97//Hs.30303:AI244662

F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, com
plete cds//2.7e-51:534:74//Hs.27007:AF060219

F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7
e-16:474:60//Hs.21264:AB018325

F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP
)//4.4e-16:428:60//Hs.155481:AJ006470

F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:
64//Hs.82292:D86969

F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:AI337050

F-NT2RP3001111

F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088

F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023

F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779

F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384

F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:U09367

F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:AB018318

F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.77637:M74297

F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305

F-NT2RP3001147

F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605

F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs.72160:AJ006266

F-NT2RP3001176

F-NT2RP3001214//EST//0.88:218:60//Hs.161147:AI417859

F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981

F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866

F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010

F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756

F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237

F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132

F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:293:60//Hs.32934:U27109

F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:64//Hs.107809:AB018269

F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454:72//Hs.41728:L75847

F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566
 F-NT2RP3001274
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:U44060
 F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.012:522:56//Hs.904:U84010
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:AB007920
 F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164
 F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER I SOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831
 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487
 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451
 F-NT2RP3001384//Homa sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595
 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB)

domain polypeptide)//1.0e-05:189:66//Hs.41728:L75847
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CT
 P) mRNA, 3' end//0.77:132:66//Hs.111024:L77567
 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047
 F-NT2RP3001426
 F-NT2RP3001427
 F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:
 431:91//Hs.85844:X66397
 F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNIN
 G ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393
 F-NT2RP3001447
 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.
 89631:U48508
 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212
 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323
 F-NT2RP3001459
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, compl
 ete cds//4.2e-10:168:70//Hs.32317:AF072836
 F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877
 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (T
 RC8) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA,
 complete cds//9.4e-139:743:91//Hs.85283:U36500
 F-NT2RP3001529//ESTs, Moderately similar to topoisomerase I C-terminal f
 ragment [H.sapiens]//0.28:224:65//Hs.105912:AI431328
 F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074
 F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.14

7918:U38291

F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:42
6:59//Hs.162:X16302

F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11
(Gq class)//0.049:185:65//Hs.1686:M69013

F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.
6e-51:345:82//Hs.144563:AF057280

F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688

F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349

F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435

F-NT2RP3001629

F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:2
76:97//Hs.9899:AF099149

F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173

F-NT2RP3001646

F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e
-172:816:98//Hs.159597:AJ012449

F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027

F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//9.0e-53:375:85//Hs.41127:AA555184

F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65/
/Hs.79077:D87071

F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK
757.1 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-111:518:99//Hs.20
364:AI420022

F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63
//Hs.7486:D83198

F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329

F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219

F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRE
CURSOR [D.melanogaster] //1.4e-31:191:94//Hs.131279:AA486291

F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41
:259:59//Hs.58435:AF001862

F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PR
ECURSOR [Mus musculus] //7.6e-159:747:98//Hs.6823:W18181

F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein m
RNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177

F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK
686.3 IN CHROMOSOME III [Caenorhabditis elegans] //3.5e-116:554:98//Hs.14
4332:AA046836

F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:
78//Hs.90998:D50918

F-NT2RP3001739

F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.
116549:AL009172

F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator
T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.22138:U49250

F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2
.4e-47:725:64//Hs.41688:U27193

F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mR
NA, complete cds//0.42:198:61//Hs.57783:U78525

F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1
e-153:710:98//Hs.28169:AB007928

F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.
79024:L03532

F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361

F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L4116

F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379
:58//Hs.32950:X82634

F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729

F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.
8e-35:481:67//Hs.158225:U68727

F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706

F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.elegans
]//2.9e-94:452:98//Hs.54952:AA872675

F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6
139:AL022326

F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896

F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185

F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247

F-NT2RP3001931

F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022
:268:61//Hs.106070:U22398

F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.
8e-167:815:96//Hs.15869:AB014575

F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335

F-NT2RP3001969

F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180

F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs
.155464:AF088219

F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.7508
7:X86779

F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946

F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821

F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67/
/Hs.147189:D88153

F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e-48:353:81//Hs.127507:AA993745

F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:212:83//Hs.71622:AA195155

F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]//4.2e-82:407:97//Hs.131888:AI091806

F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503

F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710

F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//0.91:194:65//Hs.1298:J03779

F-NT2RP3002081

F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.073:297:61//Hs.102732:U88153

F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256

F-NT2RP3002108

F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018

F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260

F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009

F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644

F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985

F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//3.0e-61:340:93//Hs.11379:AA594140

F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046
F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1
098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141
429:AA631915
F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA306435
F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (card
iomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656
F-NT2RP3002248
F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261
F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complet
e cds//0.42:189:62//Hs.110637:AC004080
F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139
F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386
F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//
1.3e-05:496:60//Hs.21537:X80910
F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871
F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:
462:56//Hs.143624:AF033383
F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1
.6e-65:588:75//Hs.154672:X16396
F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A)
gene//4.2e-166:770:98//Hs.6483:Y16355
F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5
e-161:911:89//Hs.2397:Z70200
F-NT2RP3002399
F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233
:94//Hs.22880:AA056274
F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9
e-140:649:99//Hs.12707:AB014578

F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310
F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108
F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0
:173:61//Hs.81234:AB007935
F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, com
plete cds//4.4e-146:763:93//Hs.57738:U35246
F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9
e-180:833:98//Hs.19542:AB018272
F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sap
iens] //1.3e-42:510:70//Hs.96759:AA469984
F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X787
06
F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054
F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919
F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.
89631:U48508
F-NT2RP3002603
F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:6
1//Hs.3845:AB014888
F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.
121287:AF029900
F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP
)//2.6e-13:441:63//Hs.155481:AJ006470
F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, compl
ete cds//1.7e-05:615:58//Hs.151518:U38847
F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308
F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo
sapiens] //4.1e-38:493:70//Hs.41086:AI337400
F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991

F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans] //1.6e-61:29
4:100//Hs.128750:AI367584

F-NT2RP3002687

F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200

F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657

F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514

F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291

F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6)
gene, partial cds//0.91:161:62//Hs.129736:AF040753

F-NT2RP3002785

F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713

F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens] //1.4e-76:42
3:93//Hs.41068:AA844350

F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete c
ds//2.2e-55:615:70//Hs.105940:AF004715

F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070

F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582

F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88
//Hs.123090:AB001895

F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040

F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8
e-181:853:98//Hs.6162:AB018314

F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765

F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila
melanogaster] //1.4e-133:645:97//Hs.3826:U69560

F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.
2e-13:594:57//Hs.74599:AB011160

F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.
76:412:57//Hs.21198:AB018262

F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870
F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997
F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703
F-NT2RP3002985//Human TFIIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935:U28838
F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308
F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083
F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446
F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749
F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609
F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928
F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079
F-NT2RP3003078
F-NT2RP3003101
F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98:88:68//Hs.99715:AA292700
F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740
F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061
F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975
F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:63//Hs.118397:AF053944
F-NT2RP3003150
F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.37138:U35376
F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.0

45:410:59//Hs.6150:AB011093

F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:
X78933

F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211

F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854

F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308

F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325

F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525

F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//
6.0e-55:587:70//Hs.109606:D44497

F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds/
/1.2e-129:617:98//Hs.155223:AF055460

F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200

F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, c
omplete cds//0.069:382:59//Hs.620:M69225

F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0
.98:261:59//Hs.30792:AF044924

F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:
694:93//Hs.11702:L36983

F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.757
89:D87953

F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947

F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1
e-91:681:80//Hs.23094:M19503

F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947

F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058

F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200

F-NT2RP3003330

F-NT2RP3003344

F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase
//1.2e-42:644:66//Hs.2638:Z28339

F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L788
33

F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//
Hs.148090:D83542

F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791

F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:9
6//Hs.21263:H16363

F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850

F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA,
complete cds//3.2e-22:430:63//Hs.113272:U90653

F-NT2RP3003411//Human metallothionein-Ie gene (hMT-Ie)//0.99:116:62//Hs.
74170:M10942

F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830

F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:
243:61//Hs.62:M93425

F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete c
ds//1.7e-182:853:98//Hs.14934:AF004828

F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2
e-175:826:98//Hs.26450:AB018268

F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98
330

F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302

F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete
cds//0.64:626:58//Hs.150828:AF038169

F-NT2RP3003552

F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:AI418322

F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365

F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311
 F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56
 741
 F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:56
 4:61//Hs.104:D14012
 F-NT2RP3003625
 F-NT2RP3003656
 F-NT2RP3003659
 F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586
 F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184
 F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mR
 NA, complete cds//0.013:190:63//Hs.44585:U58334
 F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69
 :246:62//Hs.118463:AF055000
 F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848
 F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61
 //Hs.48998:AB007865
 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.
 4e-150:700:98//Hs.48513:AB018300
 F-NT2RP3003746
 F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230
 F-NT2RP3003799
 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene ho
 molog//4.7e-41:432:73//Hs.1422:M19722
 F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (card
 iomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656
 F-NT2RP3003809//Human transcription factor, forkhead related activator 4
 (FREAC-4) mRNA, complete cds//5.1e-07:624:59//Hs.96028:AF042832

F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs.102877:U41315

F-NT2RP3003825

F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481

F-NT2RP3003831

F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:AF070611

F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268

F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:AB018343

F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243:90//Hs.124832:AA846576

F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//1.1e-107:499:99//Hs.105794:AA701659

F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:404:77//Hs.9006:AF057358

F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396

F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006

F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.93909:AF042498

F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H. sapiens]//2.8e-127:617:97//Hs.142151:AA984061

F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.155302:U57317

F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234

F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:

67//Hs.26441:AB002317

F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875

F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.100007:X76091

F-NT2RP3004093

F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258

F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390

F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLC0 F7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509

F-NT2RP3004145

F-NT2RP3004148

F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:AF032900

F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706

F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:62//Hs.101047:M31523

F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835

F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361

F-NT2RP3004242

F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240

F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140

F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067

F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.158471:AF088982

F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:
597:61//Hs.19261:AF007871

F-NT2RP3004332

F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285

F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426

F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999

F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1
098.3 IN CHROMOSOME III [Caenorhabditis elegans] //3.9e-45:337:83//Hs.141
429:AA631915

F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen a
lpha chain 1(V) chain [C.elegans] //4.3e-125:608:98//Hs.128781:AA160707

F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein
1//2.3e-141:804:90//Hs.123122:X97249

F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens] //3.2e-122:609:
96//Hs.20132:AA203113

F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.
153638:AF010403

F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.0
0023:357:59//Hs.99948:M97016

F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.
0e-124:583:99//Hs.27349:AB007917

F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.4
8:399:58//Hs.22616:AB014564

F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219

F-NT2RP3004472

F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8
e-152:715:98//Hs.5003:AB007925

F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Sa
ccharomyces cerevisiae] //4.6e-118:547:99//Hs.124768:AA307735

F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:75
2:97//Hs.158311:AB012851

F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus] //3.5e-
89:425:99//Hs.126082:AI077718

F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256

F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0
:370:59//Hs.158244:AB007948

F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.76
47:M94046

F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110

F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571

F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7
e-146:679:98//Hs.75970:AB014532

F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1
e-171:793:98//Hs.74750:AB011126

F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus
musculus] //2.2e-66:362:94//Hs.125870:AI364967

F-NT2RP3004569

F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRN
A, complete cds//3.3e-181:860:97//Hs.122752:AF026445

F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0
e-85:422:97//Hs.129928:AB007923

F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs
.72160:AJ006266

F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger prote
in, efp [H.sapiens] //6.4e-13:356:64//Hs.124138:AI266336

F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232

F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56/
/Hs.79706:U53204

F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436
 F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [B
 os taurus]//8.0e-177:827:98//Hs.118991:AA675919
 F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668
 F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495
 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-8
 3:556:85//Hs.129844:AF029761
 F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP
)//4.9e-13:441:62//Hs.155481:AJ006470
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e
 -151:720:97//Hs.159597:AJ012449
 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743
 F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:9
 9//Hs.57929:AB011538
 F-NT2RP4000111
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1
 e-115:548:98//Hs.64691:AB007952
 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:6
 3//Hs.75520:D26069
 F-NT2RP4000150
 F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3
 386:AF053356
 F-NT2RP4000159
 F-NT2RP4000167
 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6
 e-175:825:98//Hs.13999:AB014600
 F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006
 F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731